Figure 1A

SEQ ID NO:1

```
1      atgggaggag gacagtcaat aatgaagcaa tttaaaagta taattaacac gtcgcaggac
61     tttgaaaaaa gaatagaaaa gataaaaaaa gaagtaatca atgacccaga tgttaagcaa
121    tttttggaag cgcatcgagc tgaattaacg aatgctatga ttgatgaaga cttaaatgtg
181    ttacaagagt ataaagatca acaaaaacat tatgacggtc ataaatttgc tgattgtcca
241    aatttcgtaa aggggcatgt gcctgagtta tatgttgata ataaccgaat taaaatacgc
301    tatttacaat gcccatgtaa aatcaagtac gacgaagaac gctttgaagc tgagctaatt
361    acatctcatc atatgcaacg agatacttta aatgccaaat tgaaagatat ttatatgaat
421    catcgagacc gtcttgatgt agctatggca gcagatgata tttgtacagc aataactaat
481    ggggaacaag tgaaaggcct ttacctttat ggtccatttg ggacaggtaa atcttttatt
541    ctaggtgcaa ttgcgaatca gctcaaatct aagaaggtac gttcgacaat tatttatta
601    ccggaattta ttagaacatt aaaaggtggc tttaaagatg gttcttttga aaagaaatta
661    catcgcgtaa gagaagcaaa cattttaatg cttgatgata ttggggctga gaagtgact
721    ccatgggtga gagatgaggt aattggacct ttgctacatt atcgaatggt tcatgaatta
781    ccaacattct ttagttctaa ttttgactat agtgaattgg aacatcattt agcgatgact
841    cgtgatggtg aagagaagac taaagcagca cgtattattg aacgtgtcaa atctttgtca
901    acaccatact ttttatcagg agaaaatttc agaaacaatt ga
```

Figure 1B

SEQ ID NO:2

```
1      MGGGQSIMKQ FKSIINTSQD FEKRIEKIKK EVINDPDVKQ FLEAHRAELT NAMIDEDLNV
61     LQEYKDQQKH YDGHKFADCP NFVKGHVPEL YVDNNRIKIR YLQCPCKIKY DEERFEAELI
121    TSHHMQRDTL NAKLKDIYMN HRDRLDVAMA ADDICTAITN GEQVKGLYLY GPFGTGKSFI
181    LGAIANQLKS KKVRSTIIYL PEFIRTLKGG FKDGSFEKKL HRVREANILM LDDIGAEEVT
241    PWVRDEVIGP LLHYRMVHEL PTFFSSNFDY SELEHHLAMT RDGEEKTKAA RIIERVKSLS
301    TPYFLSGENF RNN
```

Figure 2A

SEQ ID NO:3 Complete genome sequence of bacteriophage 77

```
1       gatcaaaata cttggggaac ggttagggag taaacttcgc gataatttta aaaattcatg
61      tataacccc ctcttataac cattttaagg caggtgatga aatggagatt atagtcgatg
121     aaaatttagt gcttaaagaa aaagaaaggc tacaagtatt atataaagac atacctagca
181     ataaattaaa agtagttgat ggtttaatta ttcaagcagc aaggctacgt gtaatgcttg
241     attacatgtg ggaagacata aaagaaaaag gtgattatga tttatttact caatctgaaa
301     aggcgccacc atatgaaagg gaaagaccag tagccaaact atttaatgct agagatgctg
361     catatcaaaa aataatcaaa caattatcgg atttattgcc cgaagagaaa gaagacacag
421     aaacgccatc tgatgattac ctatgattag taataaatac gttgatgaat atataaattt
481     gtggaaacaa ggaaagataa ttttaaataa agaaagaatt gatctcttta attatctaca
541     aaaacatata tattcacgag atgatgtata ttttgatgaa cagaaaatcg aggattgtat
601     caaatttatt gaaaaatggt attttccaac attaccattt caaaggttta tcatagctaa
661     tatatttctt atagataaaa atacagatga agctttcttt acagaatttg ctattttcat
721     gggacgtgga ggcgggaaaa acggtctaat aagtgctatt agtgattttc tttctacgcc
781     cttacacgga gttaaagaat atcacatctc cattgttgct aatagtgaag atcaagcaaa
841     aacatcgttt gatgaaatca gaaccgtttt aatggataac aaacgaaata agacgggtaa
901     aacgccaaaa gctccttatg aagttagtaa agcaaaaata ataaaccgtg caactaaatc
961     ggttattcga tataacacat caaacacaaa aaccaaagac ggtggacgtg aggggtgtgt
1021    tatttttgat gaaattcatt atttctttgg tcctgaaatg gtaaacgtca aacgtggtgg
1081    attaggtaaa aagaaaaata gaagaacgtt ttatataagt actgatggtt ttgttagaga
1141    gggttatatc gatgcaatga agcacaaaat tgcaagtgta ttaagtggca aggttaaaaa
1201    tagtagattg tttgcttttt attgtaagtt agacgatcca aaagaagttg atgacagaca
1261    gacgtgggaa aaggcgaacc caatgttaca taaaccgtta tcagaatacg ctaaaacact
1321    gctaagcacg attgaagaag aatataacga tttaccattc aaccgttcaa ataagcccga
1381    attcatgact aagcgaatga atttgcctga agttgacctt gaaaaagtaa tagcaccatg
1441    gaaagaaata ctagcgacta atagagagat accaaattta gataatcaaa tgtgtattgg
1501    tggtttagac tttgcaaaca ttcgagattt tgcaagtgta gggctattat tccgaaaaaa
1561    cgatgattac atttggttag gacattcgtt tgtaagacaa gggttttttgg atgatgtcaa
1621    attagaacct cctattaaag aatgggaaaa aatgggatta ttgaccattg tcgatgatga
1681    tgtcattgaa attgaatata tagttgattg gttttttaaag gctagagaaa aatatgggct
1741    tgaaaaagtc atagctgata attatagaac tgatattgta agacgtgcgt ttgaggatgc
1801    tggcataaaa cttgaagtac ttagaaatcc aaaagcaata catggattac ttgcaccacg
1861    tatcgataca atgtttgcga aacataacgt aatatatgga gacaatcctt tgatgcgttg
1921    gtttactaat aatgttgctg taaaaatcaa gccggatgga aataaagagt atatcaaaaa
1981    agatgaagtc agacgtaaaa cggatggatt catggctttt gttcacgcat tatatagagc
2041    agacgatata gtagacaaag acatgtctaa agcgcttgat gcattaatga gtatagattt
2101    ctaatagagg aggtgagaca tgagtattct agaaaagata tttaaaacta ggaaagatat
2161    aacatatatg cttgatttag atatgataga agatctatca caacaagcgt atgtgaaacg
2221    tttagcgatt gatagttgta ttgaatttgt tgcgcgagct gtcgctcaaa gtcattttaa
2281    agtattggaa ggtaatagaa ttcaaaagaa tgatgtttac tacaagttaa atataaaacc
2341    aaatactgac ttatcaagcg atagtttttg gcaacaagtt atatataaac taatttatga
2401    taacgaggtt ttaatcgtag taagtgacag caaagaatta cttatcgcag atagctttta
2461    cagagaagag tacgctttgt atgatgatat attcaaagat gtaacggtta aagattatac
2521    ttatcaacgt actttcacaa tgcaagaggt catatattta aagtacaaca acaataaagt
2581    gacacacttt gtagaaagtc tattcgaaga ttacgggaaa atattcggaa gaatgatagg
2641    tgcacaatta aaaaactatc aaataagagg gattttgaaa tctgcctcta gcgcatatga
2701    cgaaaagaat atagaaaaat tacaagcgtt cacaaataaa ttattcaata cttttaataa
```

Figure 2B

```
2761   aaatcaacta gcaatcgcgc ctttgataga aggttttgat tatgaggaat tatctaatgg
2821   tggtaagaat agtaacatgc cttttctga attgagtgag ctaatgagag atgcaataaa
2881   aaatgttgcg ttgatgattg gtatacctcc aggtttgatt tacggagaaa cagctgattt
2941   ggaaaaaaac acgcttgtat ttgagaagtt ctgtttaaca cctttattaa aaaagattca
3001   gaacgaatta aacgcgaaac tcataacaca aagcatgtat ttgaaagata caagaataga
3061   aattgtcggt gtgaataaaa aagacccact tcaatatgct gaagcaattg acaaacttgt
3121   aagttctggt tcatttacaa ggaatgaggt gcggattatg ttaggtgaag aaccatcaga
3181   caatcctgaa ttagacgaat acctgattac taaaaactac gaaaaagcta acagtggtga
3241   aaatgatgaa aaagaaaaag atgaaaacac tttgaaaggt ggtgatgaag atgaaagcgg
3301   agattaaagg cgtcatcgtt tccaacgaag ataaatgggt ttacgaaatg cttggtatgg
3361   attcgacttg tcctaaagat gttttaacac aactagaatt tagtgatgaa gatgttgata
3421   ttataattaa ctcaaatggt ggtaacctag tagctggtag tgaaatatat acacatttaa
3481   gagctcataa aggcaaagtg aatgttcgta tcacagcaat agcagcaagt gcggcatcgc
3541   ttatcgcaat ggctggtgac cacatcgaaa tgagtccggt tgctagaatg atgattcaca
3601   atccttcaag tattgcgcaa ggagaagtga aagatctaaa tcatgctgca gaaacattag
3661   aacatgttgg tcaaataatg gctgaggcat atgcggttag agctggtaaa aacaaacaag
3721   aacttataga aatgatggct aaggaaacgt ggctaaatgc tgatgaagcc attgaacaag
3781   gttttgcgga tagtaaaatg tttgaaaacg acaatatgca aattgtagca agcgatacac
3841   aagtgttatc gaaagatgta ttaaatcgtg taacagcttt ggtaagtaaa acgccagagg
3901   ttaacattga tattgacgca atagcaaata aagtaattga aaaaataaat atgaaagaaa
3961   aggaatcaga aatcgatgtt gcagatagta aattatcagc aaatggattt tcaagattcc
4021   ttttttaata caaaaatagg aggtcataaa atgactataa atttatcgga aacattcgca
4081   aatgcgaaaa acgaatttat taatgcagta acaacggtg aaccgcaaga aagacaaaat
4141   gaattgtacg gtgacatgat taaccaacta tttgaagaaa ctaaattaca agcaaaagca
4201   gaagctgaaa gagtttctag tttacctaaa tcagcacaaa ctttgagtgc aaaccaaaga
4261   aatttctta tggatatcaa taagagtgtt ggatataaag aagaaaaact tttaccagaa
4321   gaaacaattg atagaatctt cgaagattta acaacgaatc atccattatt agctgactta
4381   ggtattaaaa atgctggttt gcgtttgaag ttcttaaaat ccgaaacttc tggcgtggct
4441   gtttggggta aaatctatgg tgaaattaaa ggtcaattag atgctgcgtt cagtgaagaa
4501   acagcaattc aaaataaatt gacagcgttt gttgtttttac caaaagattt aaatgatttt
4561   ggtcctgcgt ggattgaaag atttgttcgt gttcaaatcg aagaagcatt tgcagtggcg
4621   cttgaaactg cgttcttaaa aggtactggt aaagaccaac cgattggctt aaaccgtcaa
4681   gtacaaaaag gtgtatcggt aactgatggt gcttatccag agaaagaaga acaaggtacg
4741   cttacatttg ctaatccgcg cgctacggtt aatgaattga cgcaagtgtt taaataccac
4801   tcaactaacg agaaaggtaa atcagtagcg gttaaaggta atgtaacaat ggttgttaat
4861   ccgtccgatg cttttgaggt tcaagcacag tatacacatt taaatgcaaa tggcgtatat
4921   gttactgctt taccatttaa tttgaatgtt attgagtcta cagttcaaga agcaggtaag
4981   gttttaacgt acgttaaagg tctatatgat ggttatttag ctggtggtat taatgttcag
5041   aaatttaaag aaacacttgc gttagatgat atggatttat acactgcaaa acaatttgct
5101   tacggcaaag cgaaagataa taaagttgct gctgtttgga aattagattt aaaaggacat
5161   aaaccagctt tagaagatac cgaagaaaca ctataaaatt ttatgaggtg ataaaatggt
5221   gaaatttaaa gttgttagag aatttaaaga catagagcac aatcaacaca agtacaaagt
5281   aggggagttg tatccagctg aagggtataa caatcctcgt gttgaattgt tgacaaatca
5341   aatcaaaaat aagtacgaca aagtttatat cgtacctta gataagctga caaaacaaga
5401   attattagaa ctatgcgaat cattacaaaa aaaagcgtct agttcaatgg ttaaaagtga
5461   aatcatcgac ttattgaatg gtgaagacaa tgacgattga tgatttgctt gtcaaattta
5521   aatcacttga aaagattgac cataattcag aggatgagta cttaaagcag ttgttaaaaa
5581   tgtcgtacga gcgtataaaa aatcagtgcg gagtttttga attagagaat ttaataggtc
5641   aagaattgat acttatacgc gctagatatg cttatcaaga tttattagaa cacttcaacg
5701   acaattacag acctgaaata atagattttt cgttatctct aatggaggta tcagaagatg
```

Figure 2C

```
5761   aagaaagtgt ttaagaaacc tagaattaca actaaacgtt taaatacgcg tgttcatttt
5821   tataagtata ctgaaaataa tggtccagaa gctggagaaa aagaagaaaa attattatat
5881   agctgttggg cgagtattga tggtgtctgg ttacgtgaat tagaacaagc tatctcaaac
5941   ggaacgcaaa atgacattaa attgtatatt cgtgatccgc aaggtgatta tttacccagt
6001   gaagaacatt atcttgaaat tgaatcaaga tatttcaaaa atcgtttgaa tataaagcaa
6061   gtatcaccag atttggataa taaagacttt attatgattc gcggaggata tagttcatga
6121   gtgtgaaagt gacaggtgat aaagcattag aaagagaatt agaaaaacat tttggcataa
6181   aagagatggt aaaagttcaa gataaggcgt taatagctgg tgctaaggta attgttgaag
6241   aaataaaaaa acaactcaaa ccttcagaag actcaggagc actgattagt gagattggtc
6301   gtactgaacc tgaatggata aaggggaaac gtactgttac aattaggtgg cgtgggcctt
6361   ttgaacgatt tagaatagta catttaattg aaaatggtca tgttgagaaa aagtcaggaa
6421   aatttgtaaa acctaaagct atgggtggga ttaatagagc aataagacaa gggcaaaata
6481   agtattttga gacgctaaaa agggagttga aaaaattgtg attgatattt tgtacaaagt
6541   tcatgaagtg attagtcaag acagaattat tagagagcac gtaaatatca ataatattaa
6601   gttcaataaa taccctaatg taaaagatac tgatgtacct tttattgtta ttgacgatat
6661   cgacgaccca atacctacaa cttatactga cggagatgag tgtgcatata gttatattgt
6721   ccaaatagat gtttttgtta agtacaatga tgaatataat gcgagaatca taagaaataa
6781   gatatctaat cgcattcaaa agttattatg gtctgaacta aaaatgggaa atgtttcaaa
6841   tggaaaaccg gaatatatag aagaatttaa aacatataga agctctcgcg tttacgaggg
6901   catttttat aaggaggaaa attaaatggc agtaaaacat gcaagtgcgc caaaggcgta
6961   tattaacatt actggtttag gtttcgctaa attaacgaaa gaaggcgcgg aattaaaata
7021   tagtgatatt acaaaaacaa gaggattaca aaaaattggt gttgaaactg gtggagaact
7081   aaaaacagct tatgctgatg gcggtccaat tgaatcaggg aatacagacg gagaaggtaa
7141   aatctcatta caaatgcatg cgttccctaa agagattcgc aaaattgttt ttaatgaaga
7201   ttatgatgaa gatggcgttt acgaagagaa acaaggtaaa caaaacaatt acgtagctgt
7261   atggttcaga caagagcgta aagacggtac atttagaaca gttttattac ctaaagttat
7321   gtttacaaat cctaaaatcg atggagaaac ggctgagaaa gattgggatt tctcaagtga
7381   agaggttgaa ggtgaggcac ttttcccttt agttgataat aaaaagtcag tacgtaagta
7441   tatctttgat tcagctaaca tgacaaatca tgatggagac ggtgaaaaag gcgaagaggc
7501   tttcttaaag aaaattttag gcgaagaata tactggaaac gtgacagagg gtaacgaaga
7561   aactttgtaa caaaaccggc ttcatcggaa actgcggtaa agtcggttaa tataccagat
7621   agcattaaaa cacttaaagt tggcgacaca tacgatttaa atgttgtagt agagccatct
7681   aatcaaagta agttattgaa atacacaaca gatcaaacga atattgtatc aatcaatagt
7741   gatggtcaag ttactgcgga agcacaaggc attgctacgg ttaaagcaac agttggtaat
7801   atgagtgaca ctataacaat aaatgtagaa gcataagagg gggcaacccc tctatttat
7861   ttgaaaataa ggagagtatt ataaaatggc aaaattaaaa cgtaacatta ttcaattagt
7921   agaagatcca aaagcaaatg aaattaaatt acaaacgtac ttaacaccac acttcatttc
7981   atttgaaatt gtatacgaag caatggattt aatcgatgat attgaggacg aaaatagcac
8041   gatgaagcca agagaaatcg ctgacagatt gatggatatg gttgtaaaaa tttacgataa
8101   ccaattcaca gttaaagacc taaaagaacg tatgcatgca cctgatggaa tgaatgcact
8161   tcgtgaacaa gtgattttca ttactcaagg tcaacaaact gaggaaacta gaaatttat
8221   ccagaacatg aaataaagcc tgaagattta acatataaag caatgttgaa aaatatggat
8281   actctcatga tggacttaat tgaaaatggt aaagacgcta acgaagtttt aaaaaatgcca
8341   tttcattatg tgctttccat atatcaaaat aaaaataatg acatttctga agaaaaagca
8401   gaggctttaa ttgatgcatt ttaaccttaa ccgtttggtt agggttattt ttttgaactt
8461   ttttagaaag gaggtaaaaa atgggagaaa gaataaaaag tttatctata ggtttggatt
8521   tagatgcagc aaatttaaat agatcatttg cagaaatcaa acgaaacttt aaaactttaa
8581   attctgactt aaaaattaaca ggcaacaact tcaaatatac cgaaaaatca actgatagtt
8641   acaaacaaag gattaaagaa cttgatggaa ctatcacagg ttataagaaa aacgttgatg
8701   atttagccaa gcaatatgac aaggtatctc aagaacaggg cgaaaacagt gcagaagctc
```

Figure 2D

```
8761    aaaagttacg acaagaatat aacaaacaag caaatgagct gaattatta  gaaagagaat
8821    tacaaaaaac atcagccgaa tttgaagagt tcaaaaaagc tcaagttgaa gctcaaagaa
8881    tggcagaaag tggctgggga aaaaccagta aagttttga  aagtatggga cctaaattaa
8941    caaaaatggg tgatggttta aaatccattg gtaaaggttt gatgattggt gtaactgcac
9001    ctgtttagg  tattgcagca gcatcaggaa aagctttgc  agaagttgat aaaggtttag
9061    atactgttac tcaagcaaca ggcgcaacag gcagtgaatt aaaaaaattg cagaactcat
9121    ttaaagatgt ttatggcaat tttccagcag atgctgaaac tgttggtgga gtttaggag
9181    aagttaatac aaggttaggt tttacaggta aagaacttga aaatgccaca gagtcattct
9241    tgaaattcag tcatataaca ggttctgacg gtgtgcaagc cgtacagtta attacccgtg
9301    caatgggcga tgcaggtatc gaagcaagtg aatatcaaag tgttttggat atggtagcaa
9361    aagcggcgca agctagtggg ataagtgttg atacattagc tgatagtatt actaaatacg
9421    gcgctccaat gagagctatg ggctttgaga tgaaagaatc aattgcttta ttctctcaat
9481    gggaaaagtc aggcgttaat actgaaatag cattcagtgg tttgaaaaaa gctatatcaa
9541    attggggtaa agctggtaaa aacccaagag aagaatttaa gaagacatta gcagaaattg
9601    aaaagacgcc ggatatagct agcgcaacaa gtttagcgat tgaagcattt ggtgcaaagg
9661    caggtcctga tttagcagac gctattaaag gtggtcgctt tagttatcaa gaatttttaa
9721    aaactattga agattcccaa ggcacagtaa accaaacatt taaagattct gaaagtggct
9781    ccgaaagatt taaagtagca atgaataaat taaaattagt aggtgctgat gtatgggctt
9841    ctattgaaag tgcgtttgct cccgtaatgg aagaattaat caaaaagcta tctatagcgg
9901    ttgattggtt ttccaattta agtgatggtt ctaaaagatc aattgttatt ttcagtggta
9961    ttgctgctgc aattggtcct gtagttttg  ggttaggtgc atttataagt acaattggca
10021   atgcagtaac tgtattagct ccattgttag ctagtattgc aaaggctggt ggattgatta
10081   gttttttatc gactaaagta cctatattag gaactgtctt cacagcttta actggtccaa
10141   ttggcattgt attaggtgta ttggctggtt tagcagtcgc atttacaatt gcttataaga
10201   aatctgaaac atttagaaat tttgttaatg gtgcaattga aagtgttaaa caaacattta
10261   gtaatttat  tcaatttatt caacctttcg ttgattctgt taaaaacatc tttaaacaag
10321   cgatatcagc aatagttgat ttcgcaaaag atatttggag tcaaatcaat ggattcttta
10381   atgaaaacgg aatttccatt gttcaagcac ttcaaaatat atgcaacttt attaaagcga
10441   tatttgaatt tattttaaat tttgtaatta aaccaattat gttcgcgatt tggcaagtga
10501   tgcaatttat ttggccggcg gttaaagcct tgattgtcag tacttgggag aacataaaag
10561   gtgtaataca aggtgcttta aatatcatac ttggcttgat taagttcttc tcaagtttat
10621   tcgttggtga ttggcgagga gtttgggacg ccgttgtgat gattcttaaa ggagcagttc
10681   aattaatttg gaatttagtt caattatggt ttgtaggtaa aatacttggt gttgttaggt
10741   actttggcgg gttgctaaaa ggattgatag caggaatttg ggacgtaata agaagtatat
10801   tcagtaaatc tttatcagca atttggaatg caacaaaaag tatttttgga tttttatta
10861   atagcgtaaa atcaattttc acaaatatga aaaattggtt atctaatact tggagcagta
10921   tccgtacgaa tacaatagga aaagcgcagt cattatttag tggcgtcaaa tcaaaattta
10981   ctaatttatg gaatgcgacg aaagaaattt ttagtaattt aagaaattgg atgtcaaata
11041   tttggaattc cattaaagat aatacggtag gaattgcaag ccgtttatgg agtaaggtac
11101   gtggaatttt cacaaatatg cgcgatggct tgagttccat tatagataag attaaaagtc
11161   atatcggcgg tatggtaagc gctattaaaa aaggacttaa taaattaatc gacggtttaa
11221   actgggtcgg tggtaagttg ggaatggata aaatacctaa gttacacact ggtacagagc
11281   acacacatac tactacaaga ttagttaaga acggtaagat tgcacgtgac acattcgcta
11341   cagttgggga taagggacgc ggaaatggtc caaatggttt tagaaatgaa atgattgaat
11401   tccctaacgg taaacgtgta atcacaccta atacagatac taccgcttat ttacctaaag
11461   gctcaaaagt atacaacggt gcacaaactt attcaatgtt aaacggaacg cttccaagat
11521   ttagtttagg tactatgtgg aaagatatta aatctggtgc atcatcggca tttaactgga
11581   caaaagataa aataggtaaa ggtaccaaat ggcttggcga taaagttggc gatgtttag
11641   attttatgga aaatccaggc aaacttttaa attatatact tgaagctttt ggaattgatt
11701   tcaattcttt aactaaaggt atgggaattg caggcgacat aacaaaagct gcatggtcta
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Figure 2E

```
11761    agattaagaa  aagtgctact  gattggataa  aagaaaattt  agaagctatg  ggcggtggcg
11821    atttagtcgg  cggaatatta  gaccctgaca  aaattaatta  tcattatgga  cgtaccgcag
11881    cttataccgc  tgcaactgga  agaccatttc  atgaaggtgt  cgattttcca  tttgtatatc
11941    aagaagttag  aacgccgatg  ggtggcagac  ttacaagaat  gccatttatg  tctggtggtt
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Figure 2F

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Figure 2G

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17881   agctaatttg catattactt ctgctggcac aattgggcgt tcgacatcag cgcgtaaata
17941   caagttatct atcgaaaatc aatataacga tagagatgaa caactggaac attcaaaagc
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Figure 2H

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21361   taacagttta cggggtgctt ttatgttata attgctttta tatagtagga gtgaactata
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Figure 2I

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24721   aaaaatactt cttcatgcaa tatgtcatca tataattctt ctcctatgcc agcaccagtt
24781   gcaccacatg caatatacga tactagttta gactctttat attcatctat agaaagtgact
24841   ttattctgtt catctaattg ctcatttgca tagttaagta cgtttttcttg gcggggaggt
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25321   ttatagttca aatgtttgaa cttaggaggt gattatttga atactaatac aactttgat
25381   ttttcgttat tgaacggtaa gatagtcgaa gtgtactcga cacaatttaa ctttgctata
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25861   ttagacaagc ttaacggtgt tgaaagcgat aacaaagtta ctgatttaac agagtggcgg
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26461   acattaaaag atccagacta catcattaca gtgttgactg agtataagaa agaaaaagag
26521   caaaacttac ttttacaaca gcaagtagaa gttaacaaac caaaagtatt attcgctgac
26581   tcggtagctg gtagtgataa ttcaatactt gttggagaac tagcgaaaat acttaaacaa
26641   aacggtgttg atataggaca aaacagattg ttcaaatggt taagaaataa tggatatctc
26701   attaaaaaga gtggagaaag ttataactta ccaactcaaa agagtatgga tctaaaaatc
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Figure 2J

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26881   acatcttaaa  aggaggaaca  caatggaaca  aatcacatta  accaaagaag  agttgaaaga
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27901   atgcttaaat  acggatttga  agaaaataca  gattacacag  ctatcgctca  aaaaagagca
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29521   cagacgaaca  ggacagacta  attaacttag  tcatgaaatg  gtaggaggtc  gctatgaagc
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29641   ctgataacaa  ttcagatatt  agttactcca  caaatagaaa  tagagctagg  gagtttaacg
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Figure 2K

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29881   tataaatttg cagtatacgg aaaaattggc tcaggaaaaa ccacgtttgc tacaagagat
29941   aaagacgctt tcgtcattga cattaacgaa ggtggaacaa cggttactga cgaaggatca
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30061   ttacaggaga tgagagaaaa cggacaagaa atcaatgttg tagttattga aactattcaa
30121   aaacttagag atatgacatt gaatgatgtg atgaaaaata agtctaaaaa accaacgttt
30181   aatgattggg gagaagttgc tgaacgaatt gtcagtatgt acagattaat aggaaaactt
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30421   aacggagaaa agaaagctag atatattcta aacgctgaac cttctaatac gtttgaaaca
30481   aagattagac attcaccttc aataacaatt aacaataaga aatttgcaaa tcctagcatt
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30601   aattatgaaa atcacaggac aagcgcaatt tactaaagaa acaaatcaag aaaagtttta
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30721   caatgataga gaaaatagat atttcacaat cgtatttgaa aatgatgaag gcaaacaata
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31141   agatttagcg tttttaaggtg tggtttaaat gcaatacatt acaagatacc agaaagataa
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31621   tcacgcagac ctggcacatt atgaagcagt cggcagaggc atgaacagaa acaaaatgaa
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32641   ctttgaattt ttcaaattct acttctcttt gataaataac tttatccaca taaaggtgga
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Figure 2L

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32941   aaagttactt tttgcagaaa taacatcttt aagtaacaaa tacggatact gcacagcaag
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33241   tattaataat acaagtaata acaatataaa tagaatagat atattgtcgg gcaacccgac
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Figure 2M

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37561   ctagtgcgta  taacggtaat  gacacagagg  ggttgctaaa  agagattgag  gacgtgtata
37621   agaaagcgca  agcgtttgat  gaaatacttg  agggaatgac  aaatgctatt  caacattcag
37681   ttaaagaagg  tattgaactt  gatgaagcag  tagggattat  ggcaggtcaa  gttgtctata
37741   aatatgagga  ggaataggaa  aatgactaac  acattacaag  taaaactatt  atcaaaaaat
37801   gctagaatgc  ccgaacgaaa  tcataagacg  gatgcaggtt  atgacatatt  ctcagctgaa
37861   actgtcgtac  tcgaaccaca  agaaaaagca  gtgatcaaaa  cagatgtagc  tgtgagtata
37921   ccagagggct  atgtcggact  attaactagt  cgtagtggtg  taagtagtaa  aacgtattta
37981   gtgattgaaa  caggcaagat  agacgcggga  tatcatggca  atttagggat  taatatcaag
38041   aatgatgaag  aacgtgatgg  aatacccttt  ttatatgatg  atatagacgc  tgaattagaa
38101   gatggattaa  taagcatttt  agatataaaa  ggtaactatg  tacaagatgg  aagaggcata
38161   agaagagttt  accaaatcaa  caaaggcgat  aaactagctc  aattggttat  cgtgcctata
38221   tggacaccgg  aactaaagca  agtggaggaa  ttcgaaagtg  tttcagaacg  tggagcaaaa
38281   ggcttcggaa  gtagcggagt  gtaaagacat  cttagatcga  gttaaggagg  ttttggggaa
38341   gtgacgcaat  acttagtcac  aacattcaaa  gattcaacag  gacgaccaca  tgaacatatt
38401   actgtggcta  gagataatca  gacgtttaca  gttattgagg  cagagagtaa  agaagaagcg
38461   aaagagaagt  acgaggcaca  agttaaaaga  gatgcagtta  ttaaagtggg  tcagttgtat
38521   gaaaatataa  gggagtgtgg  gaaatgacgg  atgttaaaat  taaaactatt  tcaggtggag
38581   tttattttgt  aaaaacagct  gaacctttg  aaaaatatgt  tgaaagaatg  acgagtttta
38641   atggttatat  ttacgcaagt  actataatca  agaaaccaac  gtatattaaa  acagatacga
38701   ttgaatcaat  cacacttatt  gaggagcatg  ggaaatgaat  cagctgagaa  ttttattaca
```

Figure 2N

```
38761   tgacggtagt agtttgatat tacatgaaga tgaattattt aacgaaatag tatttgtttt
38821   ggacaatttt agaaatgatg atgactattt aacgatagaa aaagattatg gcagagaact
38881   tgtattgaac aaaggttata tagttgggat caatgttgag gaggcagatg atgattaaca
38941   tacctaaaat gaaattcccg aaaaagtaca ctgaaataat caaaaaatat aaaaataaag
39001   cacctgaaga aaaggctaag attgaagatg attttattaa agaaattaaa gataaagaca
39061   gtgaatttta cagtcctacg atggctaata tgaatgaata tgaattaagg gctatgttaa
39121   gaatgatgcc tagtttaatt gatactggag atgacaatga tgattaaaaa acttaaaaat
39181   atggatgggt tcgacatctt tattgttgga atactgtcat tattcggtat attcgcattg
39241   ctacttgtta tcacattgcc tatctataca gtggctagtt accaacacaa agaattacat
39301   caaggaacta ttacagataa atataacaag agacaagata aagaagacaa gttctatatt
39361   gtattagaca acaaacaagt cattgaaaat tccgacttat tattcaaaaa gaaatttgat
39421   agcgcagata tacaagctag gttaaaagta ggcgataagg tagaagttaa aacaatcggt
39481   tatagaatac acttttttaaa tttatatccg gtcttatacg aagtaaagaa ggtagataaa
39541   caatgattaa acaaatacta agactattat tcttactagc aatgtatgag ttaggtaagt
39601   atgtaactga gcaagtgtat attatgatga cggctaatga tgatgtagag gcgccgagtg
39661   attacgtctt tcgagcggag gtgagtgaat aatgagaata tttatttatg atttgatcgt
39721   tttgctgttt gctttcttaa tatccatata tattattgat gatggagtga taataaatgc
39781   attaggaatt tttggtatgt ataaaattat agattccttt tcagaaaata ttataaagag
39841   gtagataaaa atgaacgagc aaataatagg aagcatatat actttagcag gaggtgttgt
39901   gctttattca gttaaagaga ttttttaggta ttttacagat tctaacttac aacgtaaaaa
39961   aatcaattta gaacaaatat atccgatata tttagattgt tttaaaaagg ctaaaaagat
40021   gattggagct tatattattc caacagaaca gcatgaattt ttagattttt ttgatattga
40081   agtctttaat aatttagata agcaaagtaa aaaagcgtat gaaaatgtta ttggatttag
40141   acaaatgatt aatttatcaa atagagttaa ggcaatggaa gatttttaaga tgagtttcaa
40201   caatgaattc agtacaaatc agattttttt taatccttct tttgttatgg aaacaattgc
40261   tattataaat gaatatcaaa aagatatatc ttatttaaaa aatataatta ataaaatgaa
40321   tgaaaataga gcttataatc atattgatag ttttatcact tcagagtacc gacgaaaaat
40381   aaacgattat aatctttatc ttgataaaatt tgaagaacag tttagtcaaa agtttaaaat
40441   aaacagaact tcgataaaag aaagaattat tattaatta aacaagagga gatttaaatg
40501   atgtggatta ctatgactat tgtatttgct atattgctat tagtttgtat cagtattaat
40561   agtgatcgtg caagagagat acaagcactt agatatatga atgattatct acttgatgaa
40621   gtagttaaaa ctaaagggta caacgggtta gaagaataca ggattgaatt gaagcgaatg
40681   aataacgata ttaaaaagta atttatatta tcggaggtat tgcattgaat gataaagatt
40741   gagaaacacg atatcaaaaa gcttgaagaa tacattcagc acatcgataa ctatcgaaga
40801   gagttgaaga tgcgagaata tgaattactt gaaagtcatg aaccagataa tgcgggagct
40861   ggcaaaagta atttgccggg taacccgatt gaacgatgtg caataaagaa gtttagtgat
40921   aacaggtaca atacattaag aaatatagtt aacggtgtag atagattgat aggtgaaagt
40981   gatgaggata cgcttgagtt attaaggttt agatattggg attgtcctat tggttgttat
41041   gaatgggaag atatagcaca ttactttggt acaagtaaga caagtatatt acgtagaagg
41101   aatgcactga tcgataagtt agcaaagtat attggttatg tgtagcggac ttttacccta
41161   tgtaagtccg cattaaaaca gtttattatg ttagtatcag attaatattt aaagttatta
41221   aatgctaata cgacgcatga acaagaggcg catcactatg tgatgtgtct ttttatttat
41281   gaggtatgaa catgttcaaa ctaattgtaa atacattact acacatcaag tatagatgag
41341   tcttgatact acttaagtta tataaggtga aacattatga tgactaaaga cgaacgtata
41401   cgattctata agtctaaaga atggcaaata acaagaaaaa gagtgctaga aagagataat
41461   tatgaatgtc aacaatgtaa gagagacggc aagttaacga catatgacaa aagcaagcgt
41521   aagtcgttgg atgtagatca tatattatcg ctagaacatc atccggagtt tgctcatgac
41581   ttaaacaatt tagaaacact gtgtattaaa tgtcacaaca aaaaagaaaa gagatttata
41641   aaaaaagaaa ataaatggaa agacgaaaaa tggtaaatac ccccgggtca aaaaaatcaa
41701   aagcgat
```

Figure 3

Phage: Bacteriophage 77. Minimal ORF size: 33 a.a. Orfs "with" RBS. Number of ORFs: 99.

897: Bacteriocin precursor;
803: Terminase; Inhibitor;
015: ATP-dependent CLP protease.
081: Capsid; Inhibitor;

884: Staph;
088: Staph;
082: Structural;
075: Staph;

093: Holin;
085: Aldolase; Staph;
087: Integrase; Staph;

005: Staph;
014: Anti-repressor;
012: Staph;
022: Staph;
046: Staph;
019: Antirepressor; DNA-binding; Staph;

104: Inhibitor; Staph;
038: Staph;
026: Staph;
088: Staph;
175: Staph;
018: Staph; Mito. energy transfer signature;

112: RlnB; Staph;
040: Cytochrome c signature;

102: Staph; Inhibitor;
079: Staph;
102: Staph; Inhibitor;
043: Staph; Inhibitor;

098: Staph;
050: Staph;
096: Staph;
021: dUTPase;

049: Staph;
120: Staph;
070: Staph;

Figure 4

SEQ ID NO:4 (P77ORF104)

```
1      atggtaacca aagaattttt aaaaactaaa cttgagtgtt cagatatgta cgctcagaaa
61     ctcatagatg aggcacaggg cgatgaaaat aggttgtacg acctatttat ccaaaaactt
121    gcagaacgtc atacacgccc cgctatcgtc gaatattaa
```

SEQ ID NO:5 (P77ORF104)

```
1      MVTKEFLKTK LECSDMYAQK LIDEAQGDEN RLYDLFIQKL AERHTRPAIV EY
```

Figure 5

Predicted tryptic peptide masses of conceptual ORF in Contig 1383:

1	MGGGQSIMKqfkSIINTSQDFEKrIEKikK	30
31	evindpdvkQFLEAHRaeltnamidedlnv	60
61	lqeykDQQKhydghkFADCPNFVKghvpel	90
91	yvdnnrIKirYLQCPCKikYDEERfeaeli	120
121	tshhmqrDTLNAKlkDIYMNHRdrlDVAMA	150
151	ADDICTAITNGEQVKglylygpfgtgkSFI	180
181	LGAIANQLKskKvrSTIIYLPEFIRtlkGG	210
211	FKdgsfekKlhrVReanilmlddigaeevt	240
241	pwvrDEVIGPLLHYRmvhelptffssnfdy	270
271	selehhlamtrDGEEKtkAARiierVKsls	300
301	tpyflsgenfrNN	

Tryptic peptide fragment:

GHVPELYVDNNR   Predicted peptide mass MH+ = 1413.538

STIIYLPEFIR   Predicted peptide mass MH+ = 1352.6221

SLSTPYFLSGENFR   Predicted peptide mass MH+ = 1618.7923

Figure 6A

Optimal global alignment
Sequence 1 SEQ ID NO: 6   DnaC nucleotide *B. subtilis* (1471 letters)
Sequence 2 SEQ ID NO: 7   DnaC nucleotide *S. aureus* (1513 letters)

```
seq1     1 AT-GACAGACCTTCTGAATGACCGGCTTC---CTCCGCAAAATATAGAAGCCGAACAAGC    56
           || || |||     || ||||| ||     ||||| ||| | ||||| ||||| |
seq2     1 ATGGATAGA----ATGTATGAGCAAAATCAAATGCCGCATAACAATGAAGCTGAACAGTC    56

seq1    57 CGTGTTAGGCGCTATTTTTTTACAGCC-GTCTGCTTTAACACTGGCTTCAGAAGTATTGA   115
           || |||||| | |||| || || |||| |  |||| ||| ||| || |||||| |||
seq2    57 TGTCTTAGGTTCAATTATTATAGATCCAGAATTGATTAATACT-ACTCAGGAAGTTTTGC   115

seq1   116 TTCCAGATGATTTCTATAGAATGTCCCACCAAAAAATCTATAATGCGATGCTGGTGCTCG   175
           |||| ||    || |||||     |||| ||| ||| | ||| ||| ||| ||      |
seq2   116 TTCCTGAGTCGTTTTATAGGGGTGCCCATCAACATATTTTCCGTGCAATGATGCACTTAA   175

seq1   176 GTGACCGAGGTGAACCGGTTGATCTGGTGACA--GTTACATCAGAGCTTGCGAACACAGA   233
           |||         | ||| ||||| | || |||   | |   ||| |  |   |||   ||
seq2   176 ATGAAGATAATAAAGAAATTGATGTTGTAACATTGATGGATC--AATTATCGACGGAAGG   233

seq1   234 CCTGCTGGAAGAAGTAGGCGGTATTTCATAT-TTG-ACAGATATCGCAAACTCGGTGCCG   291
            | ||| | |||| || || |||| ||| | | ||| | | || | | |  ||| | ||
seq2   234 TACGTTGAATGAAGCGGGTGGCCCGCAATATCTTGCAGAGTTATCTACAAAT--GTACCA   291

seq1   292 ACAGCGGCTAACATAGAATATTACGCGAAAATCGTTGAGGAAAAATCGATT-CTTCGCCG   350
           || || ||    || | |  | |||||| | ||| || || ||  ||  | ||   |
seq2   292 ACGACGCGAAATGTTCAGTATTATACTGATATCGTT-TCTAAGCATGCATTAAAACGTAG   350

seq1   351 ATTAATCAGAACTGCGACAACGATTGCTCAAGACGGGTATACCCGTGAGGATGAGGTCGA   410
           ||| ||    |||||| | |    ||||| || ||  | | ||||   ||| ||| | ||
seq2   351 ATTGATTCAAACTGCAGATAGTATTGCCAATGATGGATATAATGATGAACTTGAACTAGA   410

seq1   411 --GGATTTACTCAGTGAAGCGGAAAAAACGATTATGGAAGTGGCA-CAGCGCAAAAACAC   467
             |||||  | | ||||| || |||  ||| | |  | || |  |  || |  |    ||
seq2   411 TGCGATTT--TAAGTGATGCAGAACGTCGAATTTTAGAGCTATCATCTTCTCGTGAAAGC   468

seq1   468 GAGTGCCTTCCAAAATATTAAGGACGTCCTTGTCCAGACCTATGATAATATC-GAACAGC   526
           || || |||    || | |||   |  ||| |||||| | |  | || |||| |  ||
seq2   469 GA-TGGCTTTAAAGACATTCGAGACGTCTTAGGACAAGTGTATGA-AACAGCTGAAGAGC   526

seq1   527 TTTACAATCGAAAAGGTGAT--ATCA-CGGGAATTCCAACAGGGTTTACGGAGCTTGACC   583
           ||    ||| ||| |||| |  | || | || | | || | | |||||| |  | | ||||
seq2   527 TT---GATCAAAATAGTGGTCAAACACCAGGTATACCTACAGGATATCGAGATTTAGACC   583

seq1   584 GGATGACTGCGGGTTTCCAGCGCAACGACTTGATCATTGTGGCTGCCCGTCCTTCAGTAG   643
           ||||| || || ||| || ||| |  ||  | |  | || ||| || |||| || ||||
seq2   584 AAATGACAGCAGGGTTCAACCGAAATGATTTAATTATCCTTGCAGCGCGTCCATCTGTAG   643

seq1   644 GGAAAACAGCCTTTGCCCTGAACATCGCACAAAACGTGGCGAC----GAAGACCGATG-A   698
           | || || |||| ||  ||  || | || ||||||||||| || ||     ||||| |
seq2   644 GTAAGACTGCGTTCGCACTTAATATTGCACAAAAAGTTGCAACGCATGAAGA--TATGTA   701
```

Figure 6B

```
seq1   699 GAGCGTAGCGATTTTCAGTCTTGAGATGGGTGCCGAGCAGCTCGTTATGCGTATGCTCTG   758
            | |  |    ||||||   ||  |||||||||||||  ||  ||| |   |   |||||| | ||
seq2   702 TACAGTTGGTATTTTCTCGCTAGAGATGGGTGCTGATCAGTTAGCCACACGTATGATTTG   761

seq1   759 TGCCGAGGGAAATATCAATGCCCAGAATC---TCCGTACAGGTAACCTGACCGAAGAGGA   815
            |  |    ||||||| |    |         |   |  | ||||||   |||| ||  || || ||
seq2   762 TAGTTCTGGAAATGT---TGACTCAAACCGCTTAAGAACGGGTACTATGACTGAGGAAGA   818

seq1   816 TTGGGGCAAGCTGACGATGGCAATGGGAAGCCTATCGAACAGCGGGATTTACATCGATGA   875
            |||| |    |   ||  |  ||   |||  | |    ||||   |    ||||| || |||||
seq2   819 TTGGAGTCGTTTTACTATAGCGGTAGGTAAATTATCACGTACGAAGATTTTTATTGATGA   878

seq1   876 TACACCGGGTATTCGAGTGAGTGAAATCCGTGCCAAGTGCCGCCGCTTGAAGCAGGAAAG   935
            ||||||||||||||| |  |   ||| |  ||| |  || || || | ||  |||||  |||
seq2   879 TACACCGGGTATTCGAATTAATGATTTACGTTCTAAATGTCGTCGATTAAAGCAAGAACA   938

seq1   936 CGGGCTGGGCATGATTTTGATCGATTACCTGCAATTGATTCAGGGAAGCGGT---CGTTC   992
            ||  |  |  ||||||| ||||  ||   ||| |   ||  ||||||||| ||  || | |||| |
seq2   939 TGGCTTAGACATGATTGTGATTGACTACTTACAGTTGATTCAAGGTAGTGGTTCACGTGC   998

seq1   993 AAAGGACAACCGTCAGCAGGAAGTATCTGAAATTTCCCGTGAACTGAAGTCGATTGCGAG   1052
            ||  || |  |  | ||  |||||||  |||||| ||||||| |||  | | |   | | | ||
seq2   999 GTCCGATAACAGACAACAGGAAGTTTCTGAAATCTCTCGTACATTAAAAGCATTAGCCCG   1058

seq1  1053 GGAGCTGCAAGTCCCTGTTATCGCGCTTTCTCAGCTTTCCAGGGGTGTTGAGCAGCGTCA   1112
            ||  |     ||  | ||||||||| ||   |  |||| |   | | |||||||||| || || ||
seq2  1059 TGAATTAGAATGTCCAGTTATCGCATTAAGTCAGTTATCTCGTGGTGTTGAACAACGACA   1118

seq1  1113 GGATAAACGTCCGATGATGTCTGATATCCGGGAATCAGGAAGTATCGAGCAGGACGCGGA   1172
            |||||||||| |||||||  ||||||  | ||||| ||   || ||||| || || ||||
seq2  1119 AGATAAACGTCCAATGATGAGTGATATTCGTGAATCTGGTTCGATTGAGCAAGATGCCGA   1178

seq1  1173 TATTGTCGCGTTCCTTTATCGTGATGACTACT-----------------------ATGA   1208
            ||| || || ||| |  | |  |||||||||| ||||                        ||||
seq2  1179 TATCGTTGCATTCTTATACCGTGATGATTACTATAACCGTGGCGGCGATGAAGATGATGA   1238

seq1  1209 CAAAGA---------------AACCGA--GAATAAAA--ATATTATCGAAATTATTAT   1247
            | | ||                    || ||| ||  |  |||| |   ||  |||||||||| ||
seq2  1239 CGATGATGGTGGTTTCGAGCCACAAACGAATGATGAAAACGGTGAAATTGAAATTATCAT   1298

seq1  1248 CGCCAAACAGCGTAACGGCCCGGTAGGAACCGTGTCTCTTGC-GTTCGTAAAAGAATACA   1306
            || |  ||  ||||||||||||||| ||   |||  || ||||  |   ||| |   | ||| ||||| |
seq2  1299 TGCTAAGCAACGTAACGGTCCAACAGGCACAGT-TAAGTTACATTTTATGAAACAATATA   1357

seq1  1307 ACAAATTCGTCAACCTGGAACGGCGTTTTGATGACGCAGGCGTTCCGCCCGGCGCA   1362
            |  |||||    |||   | ||  ||  || ||||  |||| |   |   |       |
seq2  1358 ATAAATT----TACCGATATCG--ATTATGCACATGCAGATATGATG------TAA   1401
```

Figure 6C

SEQ ID NO:6 DnaC nucleotide *B. subtilis*

```
   1 ATGACAGACC TTCTGAATGA CCGGCTTCCT CCGCAAAATA TAGAAGCCGA
  51 ACAAGCCGTG TTAGGCGCTA TTTTTTTACA GCCGTCTGCT TTAACACTGG
 101 CTTCAGAAGT ATTGATTCCA GATGATTTCT ATAGAATGTC CCACCAAAAA
 151 ATCTATAATG CGATGCTGGT GCTCGGTGAC CGAGGTGAAC CGGTTGATCT
 201 GGTGACAGTT ACATCAGAGC TTGCGAACAC AGACCTGCTG GAAGAAGTAG
 251 GCGGTATTTC ATATTTGACA GATATCGCAA ACTCGGTGCC GACAGCGGCT
 301 AACATAGAAT ATTACGCGAA AATCGTTGAG GAAAAATCGA TTCTTCGCCG
 351 ATTAATCAGA ACTGCGACAA CGATTGCTCA AGACGGGTAT ACCCGTGAGG
 401 ATGAGGTCGA GGATTTACTC AGTGAAGCGG AAAAAACGAT TATGGAAGTG
 451 GCACAGCGCA AAAACACGAG TGCCTTCCAA AATATTAAGG ACGTCCTTGT
 501 CCAGACCTAT GATAATATCG AACAGCTTTA CAATCGAAAA GGTGATATCA
 551 CGGGAATTCC AACAGGGTTT ACGGAGCTTG ACCGGATGAC TGCGGGTTTC
 601 CAGCGCAACG ACTTGATCAT TGTGGCTGCC CGTCCTTCAG TAGGGAAAAC
 651 AGCCTTTGCC CTGAACATCG CACAAAACGT GGCGACGAAG ACCGATGAGA
 701 GCGTAGCGAT TTTCAGTCTT GAGATGGGTG CCGAGCAGCT CGTTATGCGT
 751 ATGCTCTGTG CCGAGGGAAA TATCAATGCC CAGAATCTCC GTACAGGTAA
 801 CCTGACCGAA GAGGATTGGG GCAAGCTGAC GATGGCAATG GGAAGCCTAT
 851 CGAACAGCGG GATTTACATC GATGATACAC CGGGTATTCG AGTGAGTGAA
 901 ATCCGTGCCA AGTGCCGCCG CTTGAAGCAG GAAAGCGGGC TGGGCATGAT
 951 TTTGATCGAT TACCTGCAAT TGATTCAGGG AAGCGGTCGT TCAAAGGACA
1001 ACCGTCAGCA GGAAGTATCT GAAATTTCCC GTGAACTGAA GTCGATTGCG
1051 AGGGAGCTGC AAGTCCCTGT TATCGCGCTT TCTCAGCTTT CCAGGGGTGT
1101 TGAGCAGCGT CAGGATAAAC GTCCGATGAT GTCTGATATC CGGGAATCAG
1151 GAAGTATCGA GCAGGACGCG GATATTGTCG CGTTCCTTTA TCGTGATGAC
1201 TACTATGACA AAGAAACCGA GAATAAAAAT ATTATCGAAA TTATTATCGC
1251 CAAACAGCGT AACGGCCCGG TAGGAACCGT GTCTCTTGCG TTCGTAAAAG
1301 AATACAACAA ATTCGTCAAC CTGGAACGGC GTTTTGATGA CGCAGGCGTT
1351 CCGCCCGGCG CA
```

Figure 6D

SEQ ID NO:7 DnaC nucleotide *S. aureus*

```
   1  ATGGATAGAA TGTATGAGCA AAATCAAATG CCGCATAACA ATGAAGCTGA
  51  ACAGTCTGTC TTAGGTTCAA TTATTATAGA TCCAGAATTG ATTAATACTA
 101  CTCAGGAAGT TTTGCTTCCT GAGTCGTTTT ATAGGGGTGC CCATCAACAT
 151  ATTTTCCGTG CAATGATGCA CTTAAATGAA GATAATAAAG AAATTGATGT
 201  TGTAACATTG ATGGATCAAT TATCGACGGA AGGTACGTTG AATGAAGCGG
 251  GTGGCCCGCA ATATCTTGCA GAGTTATCTA CAAATGTACC AACGACGCGA
 301  AATGTTCAGT ATTATACTGA TATCGTTTCT AAGCATGCAT TAAAACGTAG
 351  ATTGATTCAA ACTGCAGATA GTATTGCCAA TGATGGATAT AATGATGAAC
 401  TTGAACTAGA TGCGATTTTA AGTGATGCAG AACGTCGAAT TTTAGAGCTA
 451  TCATCTTCTC GTGAAAGCGA TGGCTTTAAA GACATTCGAG ACGTCTTAGG
 501  ACAAGTGTAT GAAACAGCTG AAGAGCTTGA TCAAAATAGT GGTCAAACAC
 551  CAGGTATACC TACAGGATAT CGAGATTTAG ACCAAATGAC AGCAGGGTTC
 601  AACCGAAATG ATTTAATTAT CCTTGCAGCG CGTCCATCTG TAGGTAAGAC
 651  TGCGTTCGCA CTTAATATTG CACAAAAAGT TGCAACGCAT GAAGATATGT
 701  ATACAGTTGG TATTTTCTCG CTAGAGATGG GTGCTGATCA GTTAGCCACA
 751  CGTATGATTT GTAGTTCTGG AAATGTTGAC TCAAACCGCT TAAGAACGGG
 801  TACTATGACT GAGGAAGATT GGAGTCGTTT TACTATAGCG GTAGGTAAAT
 851  TATCACGTAC GAAGATTTTT ATTGATGATA CACCGGGTAT TCGAATTAAT
 901  GATTTACGTT CTAAATGTCG TCGATTAAAG CAAGAACATG GCTTAGACAT
 951  GATTGTGATT GACTACTTAC AGTTGATTCA AGGTAGTGGT TCACGTGCGT
1001  CCGATAACGA ACAACAGGAA GTTTCTGAAA TCTCTCGTAC ATTAAAAGCA
1051  TTAGCCCGTG AATTAGAATG TCCAGTTATC GCATTAAGTC AGTTATCTCG
1101  TGGTGTTGAA CAACGACAAG ATAAACGTCC AATGATGAGT GATATTCGTG
1151  AATCTGGTTC GATTGAGCAA GATGCCGATA TCGTTGCATT CTTATACCGT
1201  GATGATTACT ATAACCGTGG CGGCGATGAA GATGATGACG ATGATGGTGG
1251  TTTCGAGCCA CAAACGAATG ATGAAAACGG TGAAATTGAA ATTATCATTG
1301  CTAAGCAACG TAACGGTCCA ACAGGCACAG TTAAGTTACA TTTTATGAAA
1351  CAATATAATA AATTTACCGA TATCGATTAT GCACATGCAG ATATGATGTA
1401  A
```

Figure 6E

Sequence 1 SEQ ID NO: 8   DnaC *B. subtilis* (490 letters)
Sequence 2 SEQ ID NO: 9   DnaC *S. aureus* (503 letters)

```
seq1      1 MTDLLNDRLPPQNIEAEQAVLGAIFLQPSALTLASEVLIPDDFYRMSHQKIYNAMLVLGD      60
            |  :      | | ||||:|||:| :  |   :    |||:|: ||| :|| |: ||:  | :
seq2      1 MDRMYEQNQMPHNNEAEQSVLGSIIIDPELINTTQEVLLPESFYRGAHQHIFRAMMHLNE      60

seq1     61 RGEPVDLVTVTSELANTDLLEEVGGISYLTDIANSVPTAANIEYYAKIVEEKSILRRLIR     120
            : :|:||: :|:    | | ||  || ::: :||| |::|| || : :: ||||:
seq2     61 DNKEIDVVTLMDQLSTEGTLNEAGGPQYLAELSTNVPTTRNVQYYTDIVSKHALKRRLIQ     120

seq1    121 TATTIAQDGYTREDEVEDLLSEAEKTIMEVAQRKNTSAFQNIKDVLVQTYDNIEQLYNRK     180
            || :|| |||   | |:: :||:||: |:|:: : :  |::|:||| | |:   |:|
seq2    121 TADSIANDGYNDELELDAILSDAERRILELSSSRESDGFKDIRDVLGQVYETAEELDQNS     180

seq1    181 GDITGIPTGFTELDRMTAGFQRNDLIIVAARPSVGKTAFALNIAQNVATKTD-ESVAIFS     239
            |   ||||: :||:||||| ||||||I|:|||||||||||||||||||| ||| |  :| |||
seq2    181 GQTPGIPTGYRDLDQMTAGFNRNDLIILAARPSVGKTAFALNIAQKVATHEDMYTVGIFS     240

seq1    240 LEMGAEQLVMRMLCAEGNINAQNLRTGNLTEEDWGKLTMAMGSLSNSGIYIDDTPGIRVS     299
            |||||:|| ||:|: ||::: |||| :||||| : |:|:| || : |:||||||||||::
seq2    241 LEMGADQLATRMICSSGNVDSNRLRTGTMTEEDWSRFTIAVGKLSRTKIFIDDTPGIRIN     300

seq1    300 EIRAKCRRLKQESGLGMILIDYLQLIQGSG-RSKDNRQQEVSEISRELKSIARELQVPVI     358
            ::|:||||||| || |:|:|||||||||||| |: |||||||||||:|::|||| |||
seq2    301 DLRSKCRRLKQEHGLDMIVIDYLQLIQGSGSRASDNRQQEVSEISRTLKALARELECPVI     360

seq1    359 ALSQLSRGVEQRQDKRPMMSDIRESGSIEQDADIVAFLYRDDYYDK--------------     404
            |||||||||||||||||||||||||||||||||||||||||||||::
seq2    361 ALSQLSRGVEQRQDKRPMMSDIRESGSIEQDADIVAFLYRDDYYNRGGDEDDDDGGFEP     420

seq1    405 ETENKN-IIEIIIAKQRNGPVGTVSLAFVKEYNKFVNLERRFDDAGVPPGA          454
            :| ::| |||||||||||| ||| | |:|:|||| :::       |
seq2    421 QTNDENGEIEIIIAKQRNGPTGTVKLHFMKQYNKFTDIDYAHADM-----M          466
```

Figure 6F

SEQ ID NO:8 DnaC *B. subtilis*

```
  1  MTDLLNDRLP PQNIEAEQAV LGAIFLQPSA LTLASEVLIP DDFYRMSHQK
 51  IYNAMLVLGD RGEPVDLVTV TSELANTDLL EEVGGISYLT DIANSVPTAA
101  NIEYYAKIVE EKSILRRLIR TATTIAQDGY TREDEVEDLL SEAEKTIMEV
151  AQRKNTSAFQ NIKDVLVQTY DNIEQLYNRK GDITGIPTGF TELDRMTAGF
201  QRNDLIIVAA RPSVGKTAFA LNIAQNVATK TDESVAIFSL EMGAEQLVMR
251  MLCAEGNINA QNLRTGNLTE EDWGKLTMAM GSLSNSGIYI DDTPGIRVSE
301  IRAKCRRLKQ ESGLGMILID YLQLIQGSGR SKDNRQQEVS EISRELKSIA
351  RELQVPVIAL SQLSRGVEQR QDKRPMMSDI RESGSIEQDA DIVAFLYRDD
401  YYDKETENKN IIEIIIAKQR NGPVGTVSLA FVKEYNKFVN LERRFDDAGV
451  PPGA
```

SEQ ID NO:9 DnaC *S. aureus*

```
  1  MDRMYEQNQM PHNNEAEQSV LGSIIIDPEL INTTQEVLLP ESFYRGAHQH
 51  IFRAMMHLNE DNKEIDVVTL MDQLSTEGTL NEAGGPQYLA ELSTNVPTTR
101  NVQYYTDIVS KHALKRRLIQ TADSIANDGY NDELELDAIL SDAERRILEL
151  SSSRESDGFK DIRDVLGQVY ETAEELDQNS GQTPGIPTGY RDLDQMTAGF
201  NRNDLIILAA RPSVGKTAFA LNIAQKVATH EDMYTVGIFS LEMGADQLAT
251  RMICSSGNVD SNRLRTGTMT EEDWSRFTIA VGKLSRTKIF IDDTPGIRIN
301  DLRSKCRRLK QEHGLDMIVI DYLQLIQGSG SRASDNRQQE VSEISRTLKA
351  LARELECPVI ALSQLSRGVE QRQDKRPMMS DIRESGSIEQ DADIVAFLYR
401  DDYYNRGGDE DDDDGGFEP QTNDENGEIE IIIAKQRNGP TGTVKLHFMK
451  QYNKFTDIDY AHADMM
```
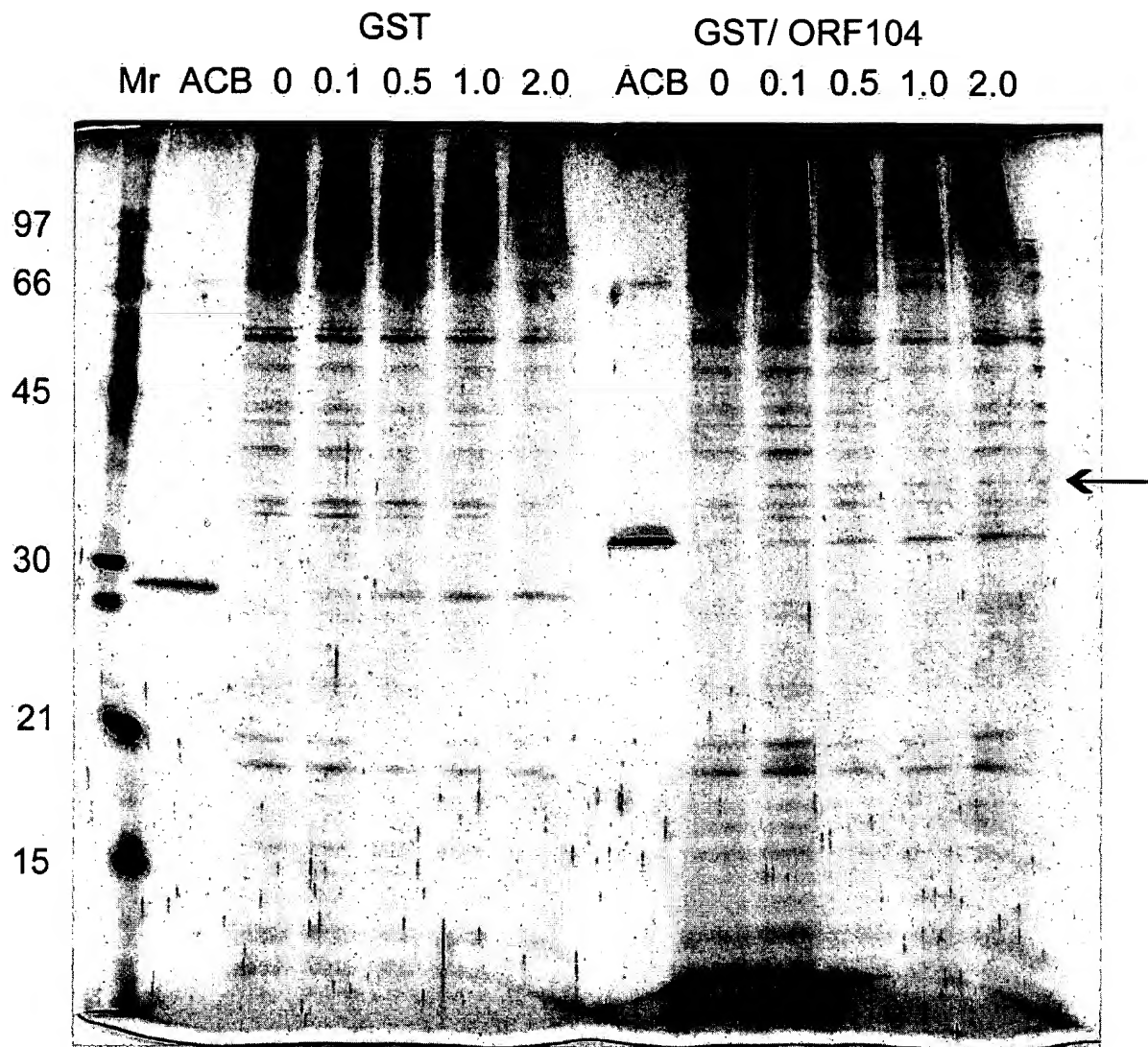
Figure 7A

Figure 7B

Figure 7C

BACTERIAL GROWTH KINETICS

NON KILLER ORF, NO INDUCTION

NON KILLER ORF, INDUCTION

77pTORF 104, NO INDUCTION

77pTORF 104, INDUCTION

CFU X 10e6 /ml

TIME (MIN.)

Figure 8A

Figure 8B

GST   GST/ ORF104

ACB 0 0.1 0.5 1.0 2.0   Mr   ACB 0 0.1 0.5 1.0 2.0
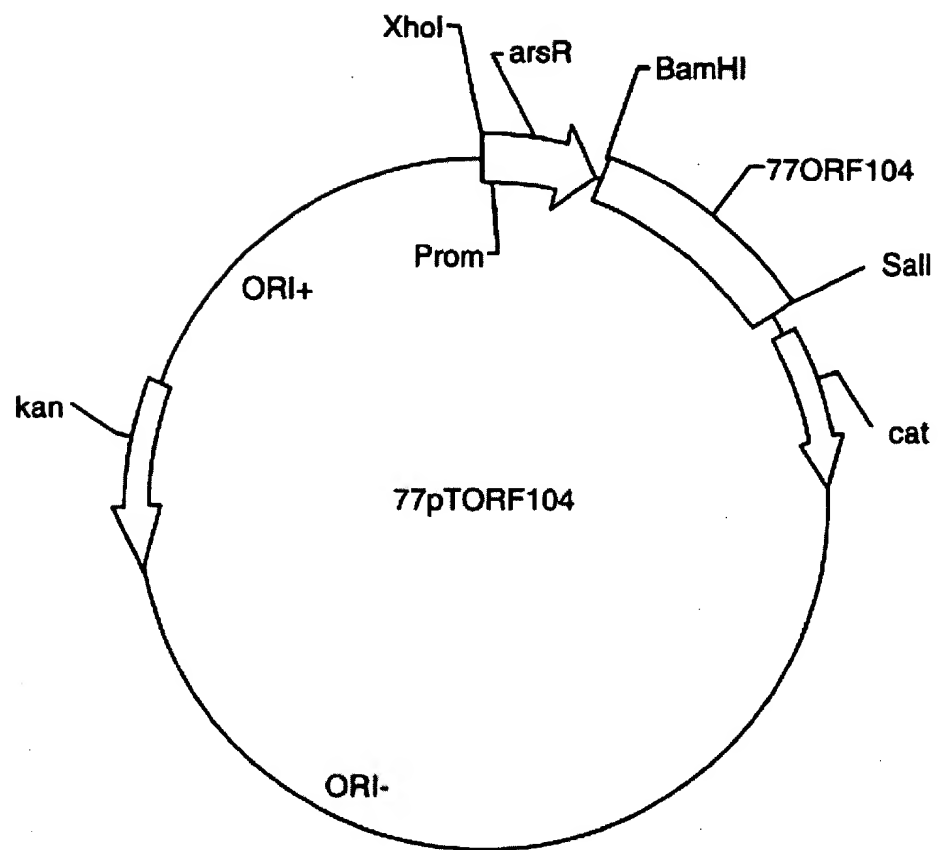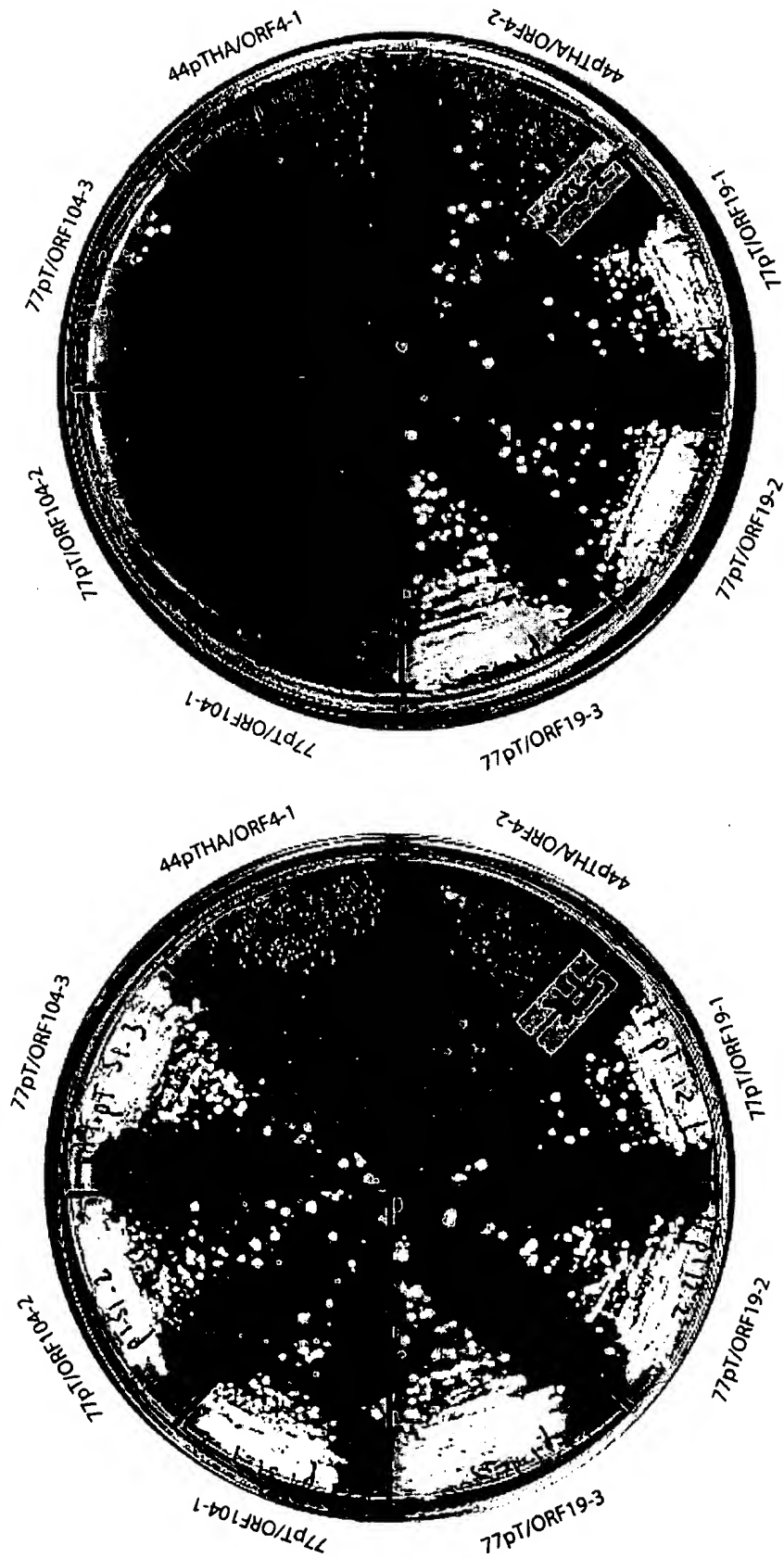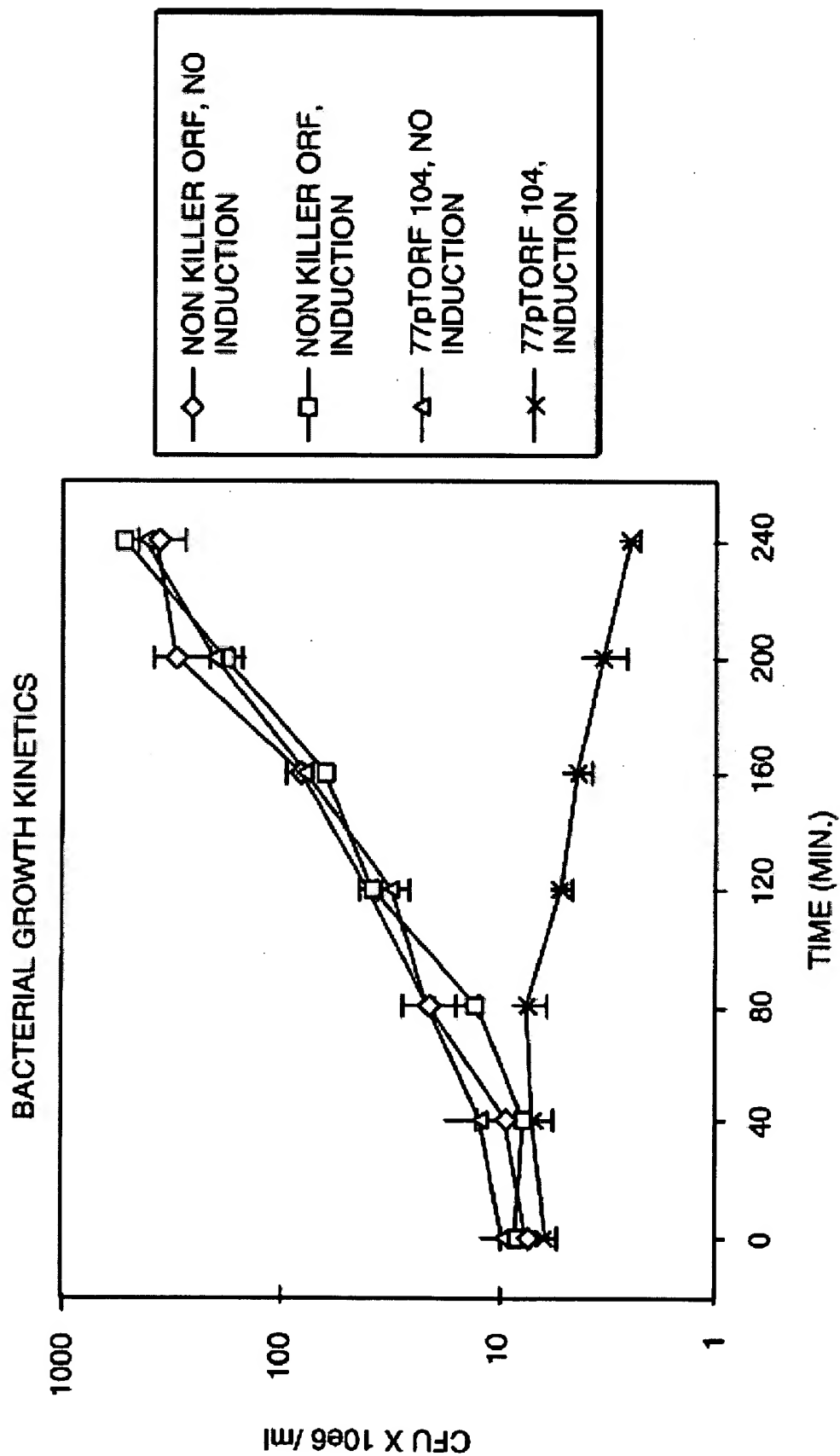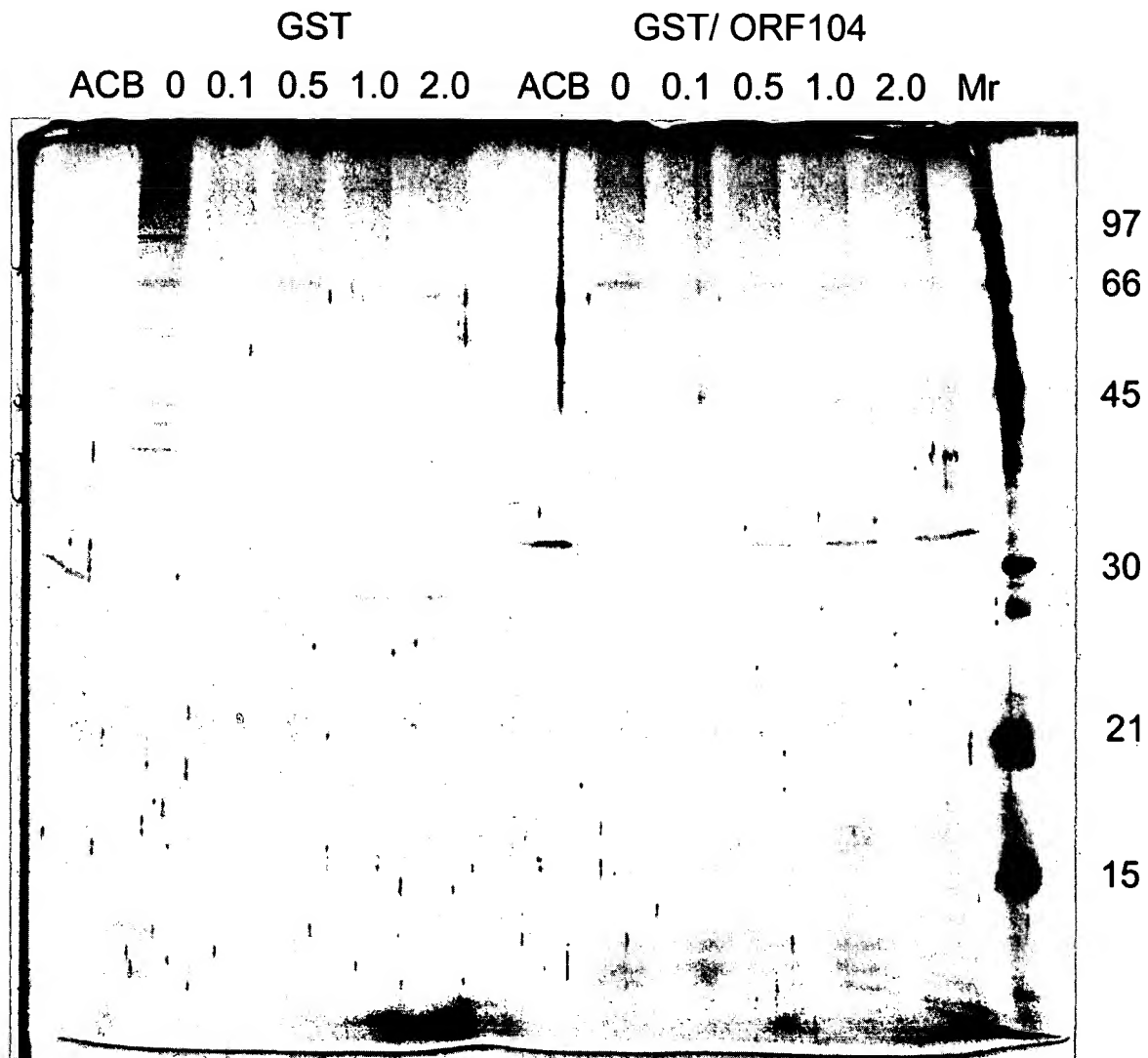
Figure 8C

Figure 8D

Figure 9

Figure 10

Lys Extract   FP/S Extract
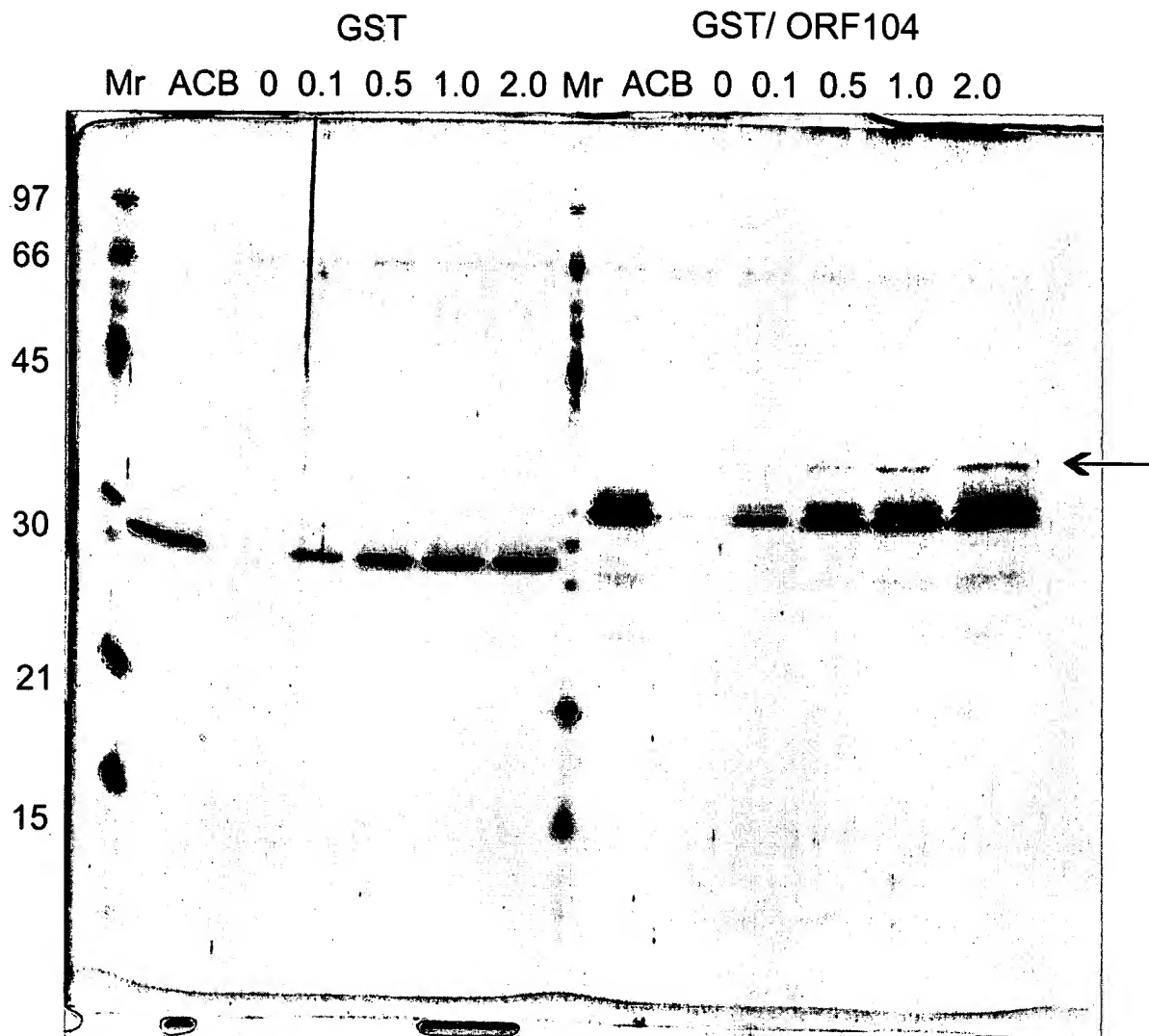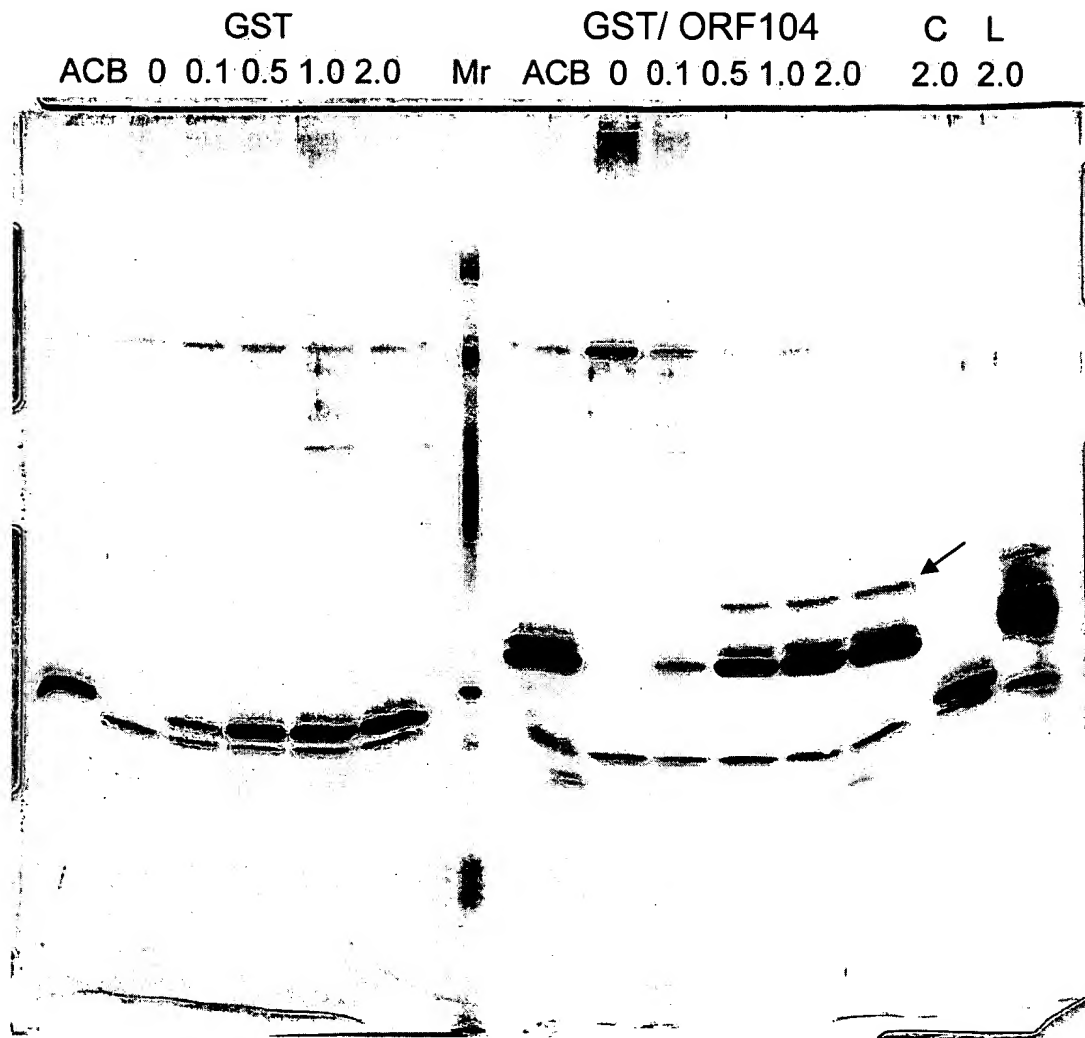
ACB 0 0.1 0.5 1.0 2.0   Mr   ACB 0 0.1 0.5 1.0 2.0
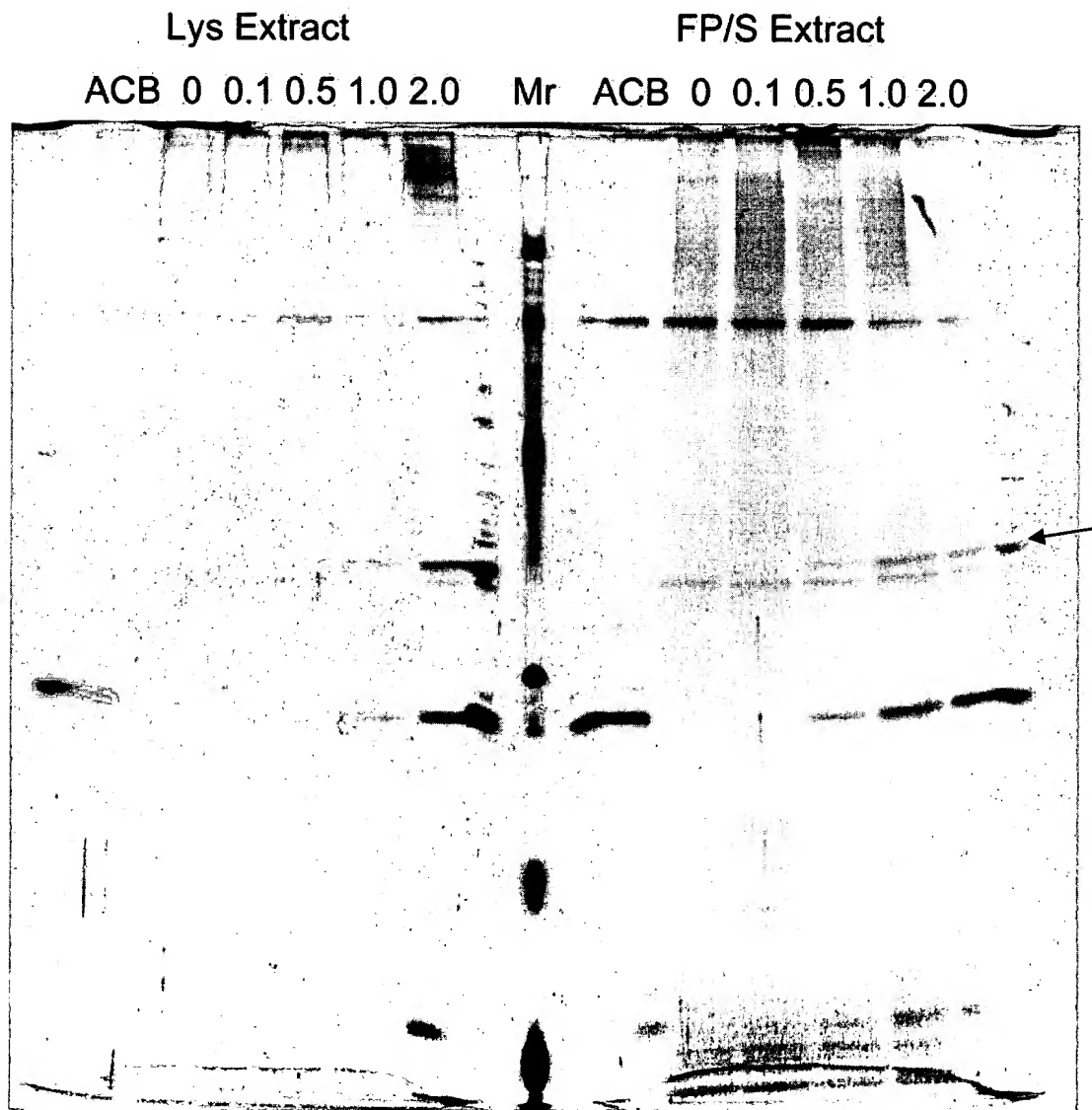
Figure 11A

Tryptic peptide mass spectrum of interacting protein (1% Triton X-100 elute)
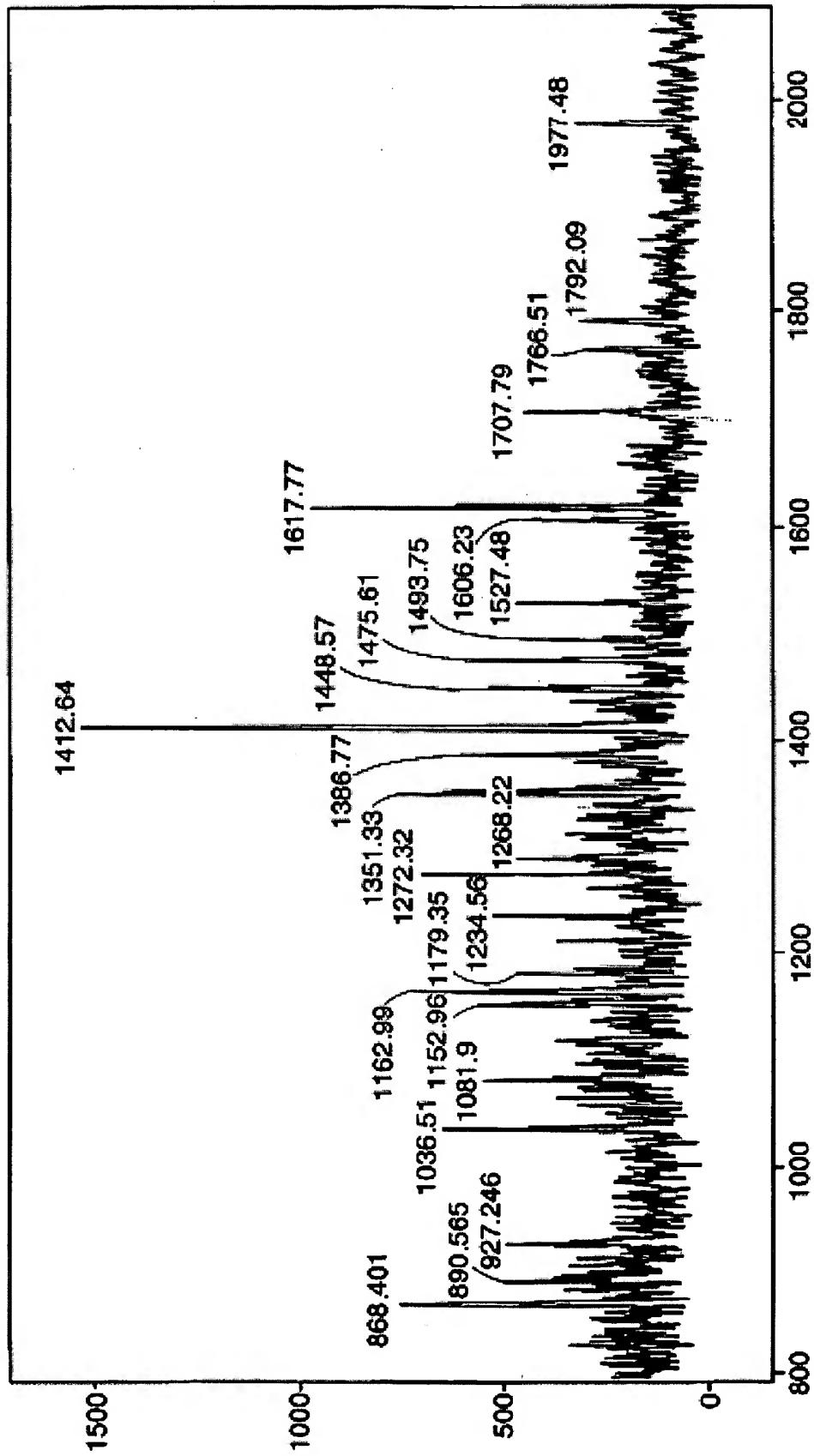
Figure 11B

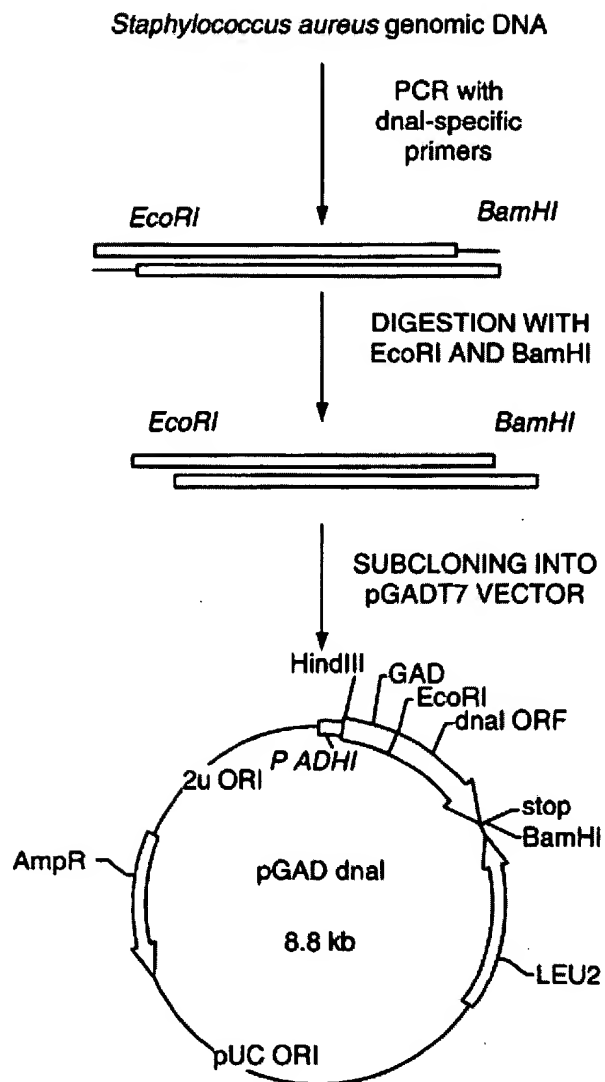Tryptic peptide mass spectrum of interacting protein (1% SDS eluate)

Figure 12A

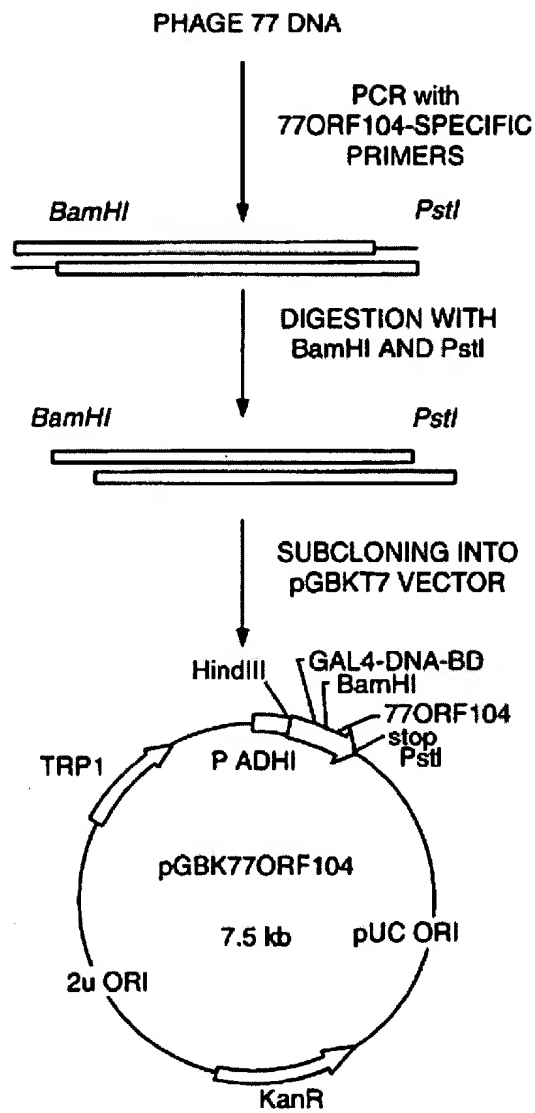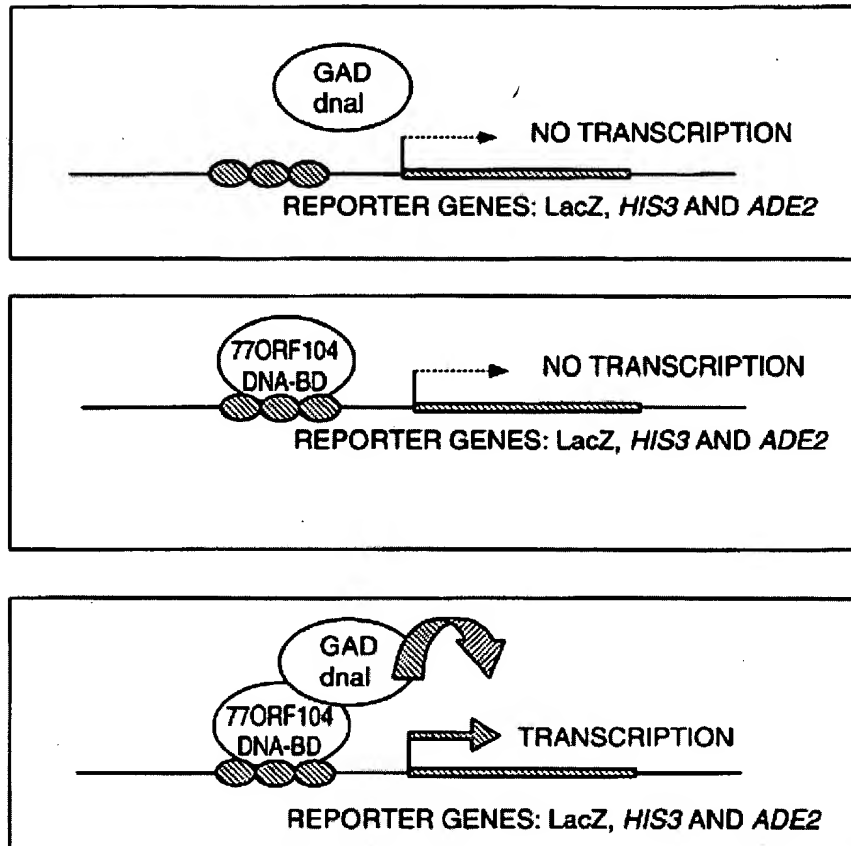Staphylococcus aureus genomic DNA

PCR with
dnaI-specific
primers

EcoRI   BamHI

DIGESTION WITH
EcoRI AND BamHI

EcoRI   BamHI

SUBCLONING INTO
pGADT7 VECTOR

HindIII   GAD
          EcoRI
          dnaI ORF

P ADHI

2u ORI

AmpR

pGAD dnaI

8.8 kb

stop
BamHI

LEU2

pUC ORI

Figure 12B

PHAGE 77 DNA

↓ PCR with
77ORF104-SPECIFIC
PRIMERS

BamHI   *PstI*

↓ DIGESTION WITH
BamHI AND PstI

BamHI   *PstI*

↓ SUBCLONING INTO
pGBKT7 VECTOR

HindIII ⌐GAL4-DNA-BD
⌐ BamHI
- 77ORF104
- stop
P ADHI   PstI
TRP1
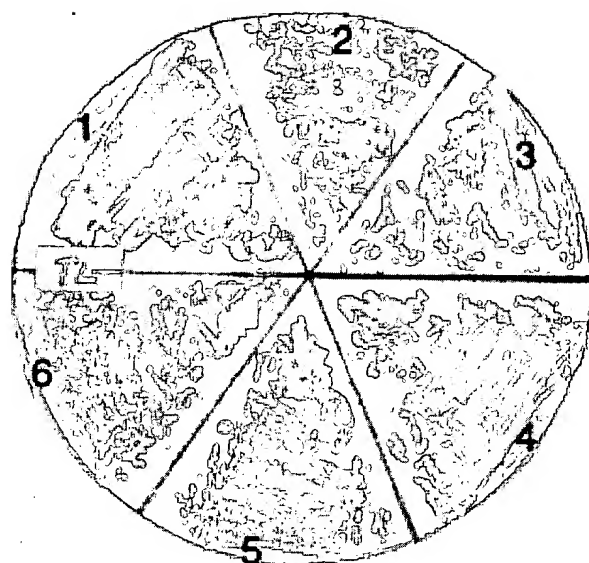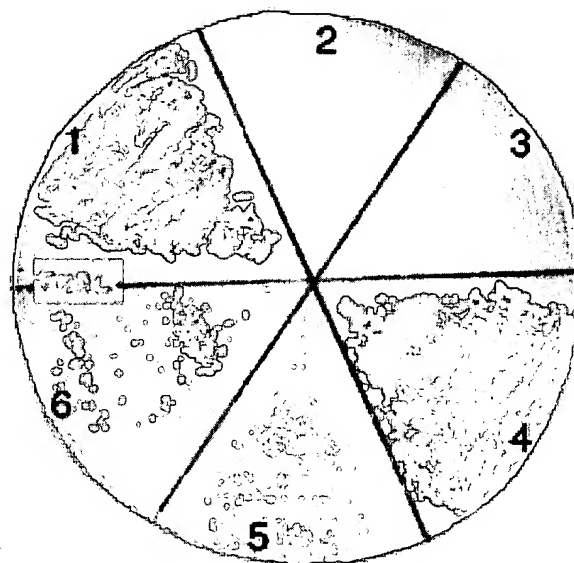pGBK77ORF104
7.5 kb   pUC ORI
2u ORI
KanR

Figure 12C

Figure 12D

SD plate without Trp and Leu   **SD plate without Trp, Leu, His and Ade**

SD: Synthetic medium, Trp: tryptophan, Leu: leucine, His: histidine, Ade: adenine

1) pGBKT7-53 and pGADT7-T
2) pGBKT7-53 and pGAD dnaI
3) pGBK77ORF104 and pGADT7-T
4) pGBKT7-LAM and pCL1
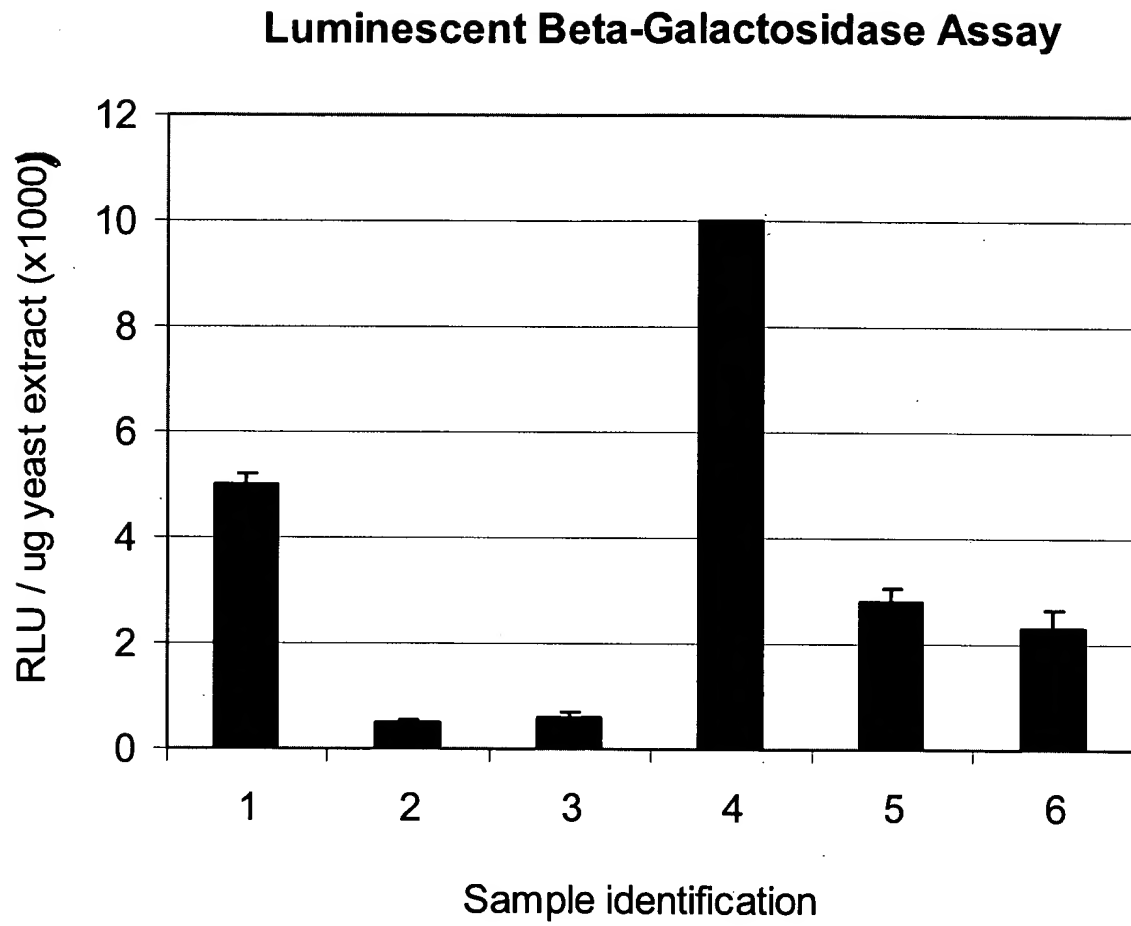5) pGBK77ORF104 and pGAD dnaI
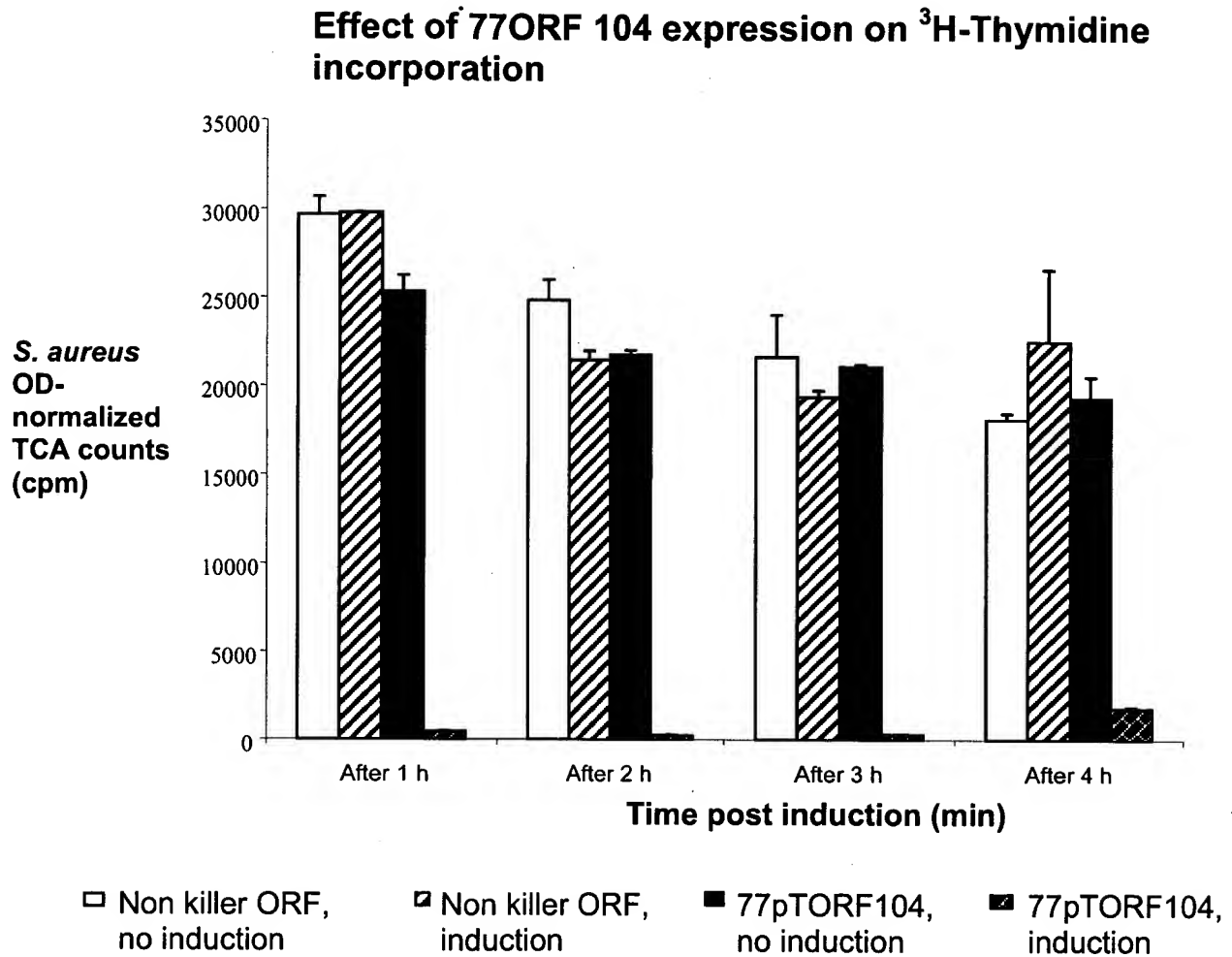6) pGBK dnaI and pGAD77ORF104

Figure 12E

Luminescent Beta-Galactosidase Assay

Sample identification

Figure 13

Effect of 77ORF 104 expression on ^{3}H-Thymidine incorporation

Legend:
□ Non killer ORF, no induction
▨ Non killer ORF, induction
■ 77pTORF104, no induction
▨ 77pTORF104, induction

FIGURE 14A

Endoproteinase Glu-C

0 mg/ml   2.0 mg/ml   ACB 2.0 mg/ml

Mr   L   FT   1   2   FT   1   2   1   2

97

66

45

V38

30

V25

V24

20

V16(-)

15

Figure 14B

Chymotrypsin
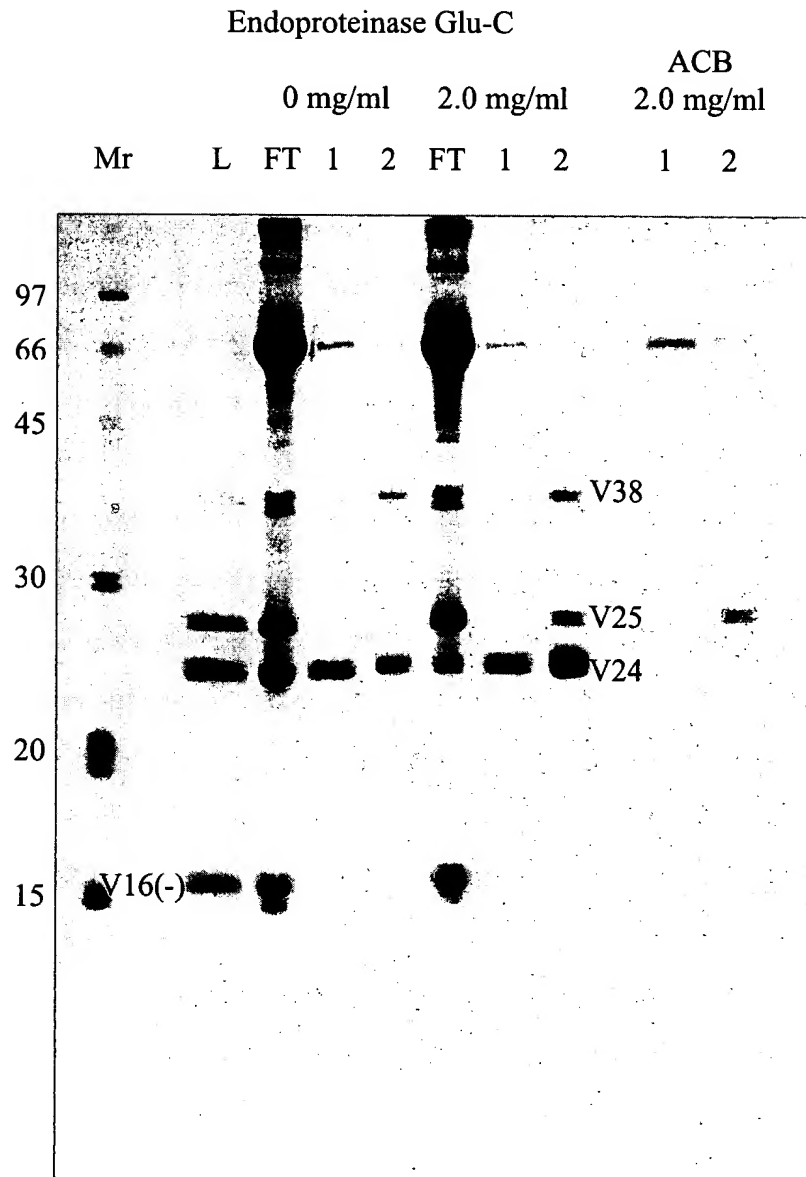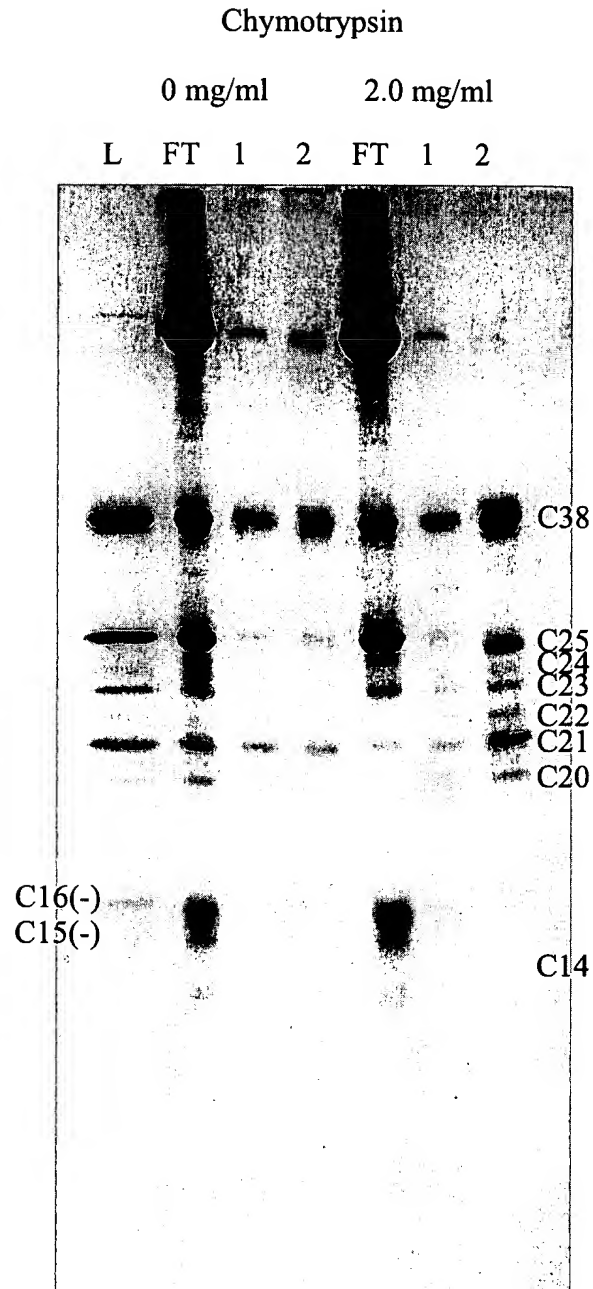
Figure 14C

Amino acid residues corresponding to interacting partial proteolytic fragments.

Protease	Proteolytic fragment ID (from Fig. 14A, B)	ID of SEQ ID NO:2 fragment interacting with 77ORF104	
		From amino	to carboxyl
Endoproteinase Glu-C	V24	117	313
	V24	119	313
Chymotrypsin	C38	12	313
	C25	83	313
	C24	77	305
	C23	77	304
	C22	116	313
	C21	131	313

SEQ ID NO:2	complete	1	313

Figure 15

SEQ ID NO: 16
>*S. aureus* DnaI: amino acid 150-313
AADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIIYLPEFIRTLKG
GFKDGSFEKKLHRVREANILMLDDIGAEEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFD
YSELEHHLAMTRDGEEKTKAARIIERVKSLSTPYFLSGENFRNN

**SEQ ID NO: 17**
>*S. aureus* dnaI: nucleotide 448-942
gcagcagatgatatttgtacagcaataactaatggggaacaagtgaaaggcctttacctt
tatggtccatttgggacaggtaaatctttattctaggtgcaattgcgaatcagctcaaa
tctaagaaggtacgttcgacaattatttatttaccggaatttattagaacattaaaaggt
ggctttaaagatggttctttttgaaaagaaattacatcgcgtaagagaagcaaacatttta
atgcttgatgatattggggctgaagaagtgactccatgggtgagagatgaggtaattgga
cctttgctacactatcgaatggttcatgaattaccaacattctttagttctaattttgac
tatagtgaattggaacatcatttagcgatgactcgtgatggtgaagagaagactaaagca
gcacgtattattgaacgtgtcaaatctttgtcaacaccatactttttatcaggagaaaat
ttcagaaacaattga

SEQ ID NO: 18
>*S. aureus* DnaI: amino acid 64-313
YKDQQKHYDGHKFADCPNFVKGHVPELYVDNNRIKIRYLQCPCKIKYDEERFEAELITSH
HMQRDTLNAKLKDIYMNHRDRLDVAMAADDICTAITNGEQVKGLYLYGPFGTGKSFILGA
IANQLKSKKVRSTIIYLPEFIRTLKGGFKDGSFEKKLHRVREANILMLDDIGAEEVTPWV
RDEVIGPLLHYRMVHELPTFFSSNFDYSELEHHLAMTRDGEEKTKAARIIERVKSLSTPY
FLSGENFRNN

Figure 16A

DnaI fragments and 77ORF104

TL minus SD medium   **THAL minus SD medium**
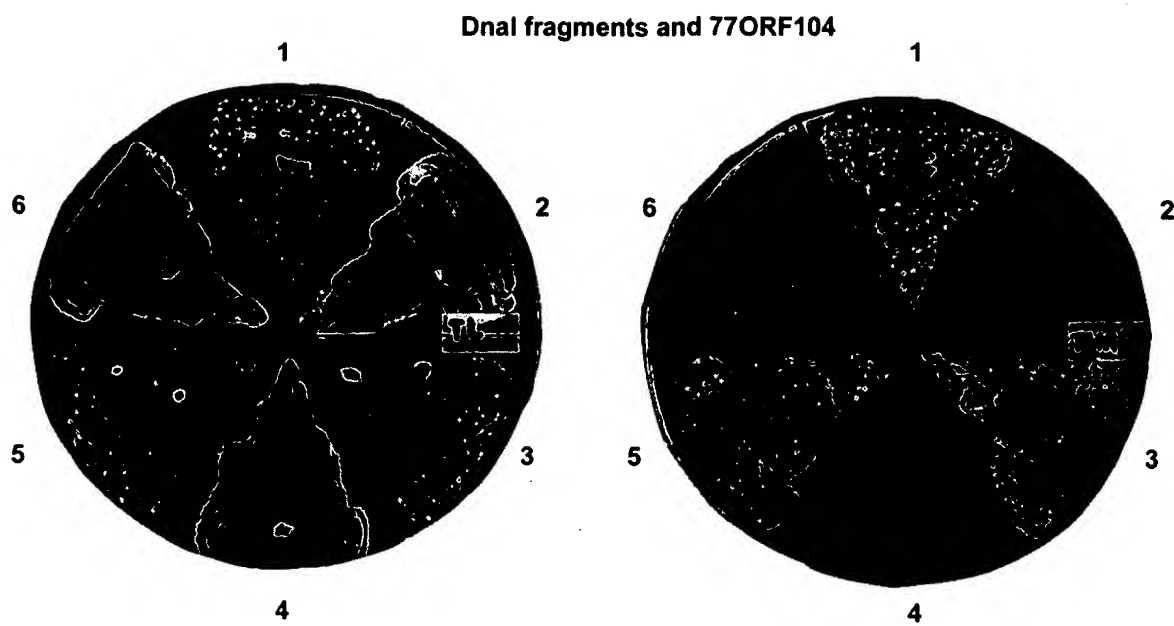
1. pGADDnaI(150-313) and pGBKORF104

2. pGADDnaI(150-313) and pGBKLam

3. pGADDnaI(64-313) and pGBKORF104

4. pGADDnaI(64-313) and pGBKLam

5. pGADDnaI and pGBKORF104

6. 77pGADORF12 and pGBKORF104

Figure 16B

Interaction
with
77 ORF 104

SEQ ID NO: 2   1 ————————————————————— 313   **Yes**

SEQ ID NO: 18   64 ————————————————— 313   **Yes**

SEQ ID NO: 16   150 ——————————— 313   **Yes**